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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:50:39 ; Search time 16.5 Seconds
(without alignments)
206.504 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIVTFTGIYSVNKEQL.....KPSDPDQHAQKYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	386	100.0	66	2	US-08-511-485-24
2	386	100.0	66	4	US-09-201-936-24
3	386	100.0	66	4	US-09-011-356-24
4	386	100.0	496	2	US-08-511-485-10
5	386	100.0	496	3	US-09-212-971-10
6	386	100.0	496	3	US-08-800-929A-10
7	386	100.0	496	4	US-09-617-053A-10
8	386	100.0	496	4	US-09-201-936-10
9	386	100.0	496	4	US-09-011-356-10
10	386	100.0	496	4	US-09-672-717-225
11	366	94.8	66	2	US-08-511-485-25
12	366	94.8	66	4	US-09-201-936-25
13	366	94.8	66	4	US-09-011-356-25
14	366	94.8	236	4	US-09-239-867-4
15	366	94.8	497	2	US-08-511-485-4
16	366	94.8	497	3	US-09-212-971-4
17	366	94.8	497	3	US-08-800-929A-4
18	366	94.8	497	4	US-09-617-053A-4
19	366	94.8	497	4	US-08-657-759-2
20	366	94.8	497	4	US-09-201-936-4
21	366	94.8	497	4	US-09-011-356-4
22	366	94.8	497	4	US-09-672-717-219
23	334	86.5	236	3	US-09-121-979-4
24	334	86.5	236	3	US-09-332-319-4
25	334	86.5	236	4	US-09-239-867-2
26	279	72.3	53	4	US-08-657-759-19
27	233	60.4	50	3	US-08-975-080-28

28	233	60.4	50	3	US-08-975-080-29	Sequence 29, Appl
29	233	60.4	50	3	US-08-975-080-32	Sequence 32, Appl
30	198	51.3	68	2	US-08-511-485-26	Sequence 26, Appl
31	198	51.3	68	4	US-09-201-936-26	Sequence 26, Appl
32	198	51.3	68	4	US-09-011-356-26	Sequence 26, Appl
33	198	51.3	604	2	US-08-511-485-6	Sequence 6, Appl
34	198	51.3	604	3	US-09-212-971-6	Sequence 6, Appl
35	198	51.3	604	3	US-08-800-929A-6	Sequence 6, Appl
36	198	51.3	604	3	US-08-569-749-4	Sequence 4, Appl
37	198	51.3	604	4	US-09-617-053A-6	Sequence 6, Appl
38	198	51.3	604	4	US-09-201-936-6	Sequence 6, Appl
39	198	51.3	604	4	US-09-011-356-6	Sequence 6, Appl
40	198	51.3	604	4	US-09-672-717-221	Sequence 221, App
41	198	51.3	604	5	PCT-US96-12860-4	Sequence 4, Appl
42	190	49.2	68	2	US-08-511-485-28	Sequence 28, Appl
43	190	49.2	68	4	US-09-201-936-28	Sequence 28, Appl
44	190	49.2	68	4	US-09-011-356-28	Sequence 28, Appl
45	190	49.2	268	3	US-08-836-134-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-24

Query Match 100.0%; Score 386; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGLTDWKPSDPDQHAQKY 60
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Db      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
QY      61 PGCKYL 66
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Db      61 PGCKYL 66

RESULT 2
US-09-201-936-24
; Sequence 24, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match      100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
        |||||
Db      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60

QY      61 PGCKYL 66
        |||||
Db      61 PGCKYL 66

RESULT 3
US-09-011-356-24
; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
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; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24

Query Match      100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
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Db      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60

QY      61 PGCKYL 66
        |||||
Db      61 PGCKYL 66

RESULT 4
US-08-511-485-10
; Sequence 10, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-10

Query Match      100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
        |||||
Db      264 YEARIVTGTTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 323

QY      61 PGCKYL 66
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Db      324 PGCKYL 329
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RESULT 5
US-09-212-971-10
; Sequence 10, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-212-971-10

Query Match      100.0%; Score 386; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 60
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Db      264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 323

QY      61 PGCKYL 66
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Db      324 PGCKYL 329

RESULT 6
US-08-800-929A-10
; Sequence 10, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-929A-10

Query Match      100.0%; Score 386; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 60
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Db      264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 323

QY      61 PGCKYL 66
      |||||
Db      324 PGCKYL 329

RESULT 7
US-09-617-053A-10
; Sequence 10, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-617-053A-10

Query Match      100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 60
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Db      264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 323
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QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 8

US-09-201-936-10
; Sequence 10, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 60
Db 264 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 9

US-09-011-356-10
; Sequence 10, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-10

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 60
Db 264 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 10

US-09-672-717-225
; Sequence 225, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-672-717-225

Query Match 100.0%; Score 386; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 60
Db 264 YEARIVTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 11

US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-25

Query Match 94.8%; Score 366; DB 2; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 12
US-09-201-936-25
Sequence 25, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60

Db 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66
RESULT 13
US-09-011-356-25
Sequence 25, Application US/09011356A
Patent No. 6656704
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.2e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 14
US-09-239-867-4
Sequence 4, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 94.8%; Score 366; DB 4; Length 236;
Best Local Similarity 95.5%; Pred. No. 5.6e-40;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 4 YEARIFTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 15
US-08-511-485-4
; Sequence 4, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-4

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.4e-39;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 265 YEARIFTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

Search completed: March 10, 2004, 13:55:49
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:09 ; Search time 49.5 Seconds
(without alignments)
376.730 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIVTFGTWYSVNKEQL.....KPSDDPDQHA KCYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	496	2	AAW19584 Mouse apo
2	386	100.0	496	2	AAW69297 Murine XI
3	386	100.0	496	5	ABG65666 Mouse inh
4	372	96.4	66	7	ADB61828 Mouse inh
5	372	96.4	496	6	ABP72157 Mouse inh
6	366	94.8	66	7	ADB61827 Rat inhib
7	366	94.8	66	7	ADB61810 Human inh
8	366	94.8	236	5	ABG32418 X-linked
9	366	94.8	278	5	AAO20511 Protein o
10	366	94.8	497	2	AAW19581 Human apo
11	366	94.8	497	2	AAW69294 Human XIA
12	366	94.8	497	3	AAW59451 Human XIA
13	366	94.8	497	3	AAW99985 Human X-1
14	366	94.8	497	5	ABG65663 Human inh
15	366	94.8	497	7	ADB80961 RING-SH c
16	357	92.5	496	2	AAW19745 Mouse inh
17	334	86.5	66	7	ADB61820 Human inh
18	334	86.5	236	3	AAW81440 Human TIA
19	334	86.5	236	4	AAE00365 Human IAP
20	334	86.5	236	5	AAU75066 Human tes
21	334	86.5	236	5	ABG32417 Inhibitor
22	334	86.5	464	5	AAU75747 Human Inh
23	328	85.0	236	4	AAE00366 Chimpanze
24	325	84.2	66	7	ADB61831 Gorilla i
25	325	84.2	236	4	AAE00367 Gorilla I

26	306	79.3	57	7	ADB61832	Adb61832 Unidentif
27	279	72.3	66	7	ADB61829	Adb61829 Chicken i
28	258	66.8	52	7	ADB61830	Adb61830 Bovine in
29	212	54.9	68	7	ADB61833	Adb61833 Zebra fis
30	198	51.3	68	7	ADB61813	Adb61813 Human inh
31	198	51.3	557	6	ABP72159	Abp72159 Inhibitor
32	198	51.3	604	2	AAW19582	Aaw19582 Human apo
33	198	51.3	604	2	AAW19747	Aaw19747 Human inh
34	198	51.3	604	2	AAW13546	Aaw13546 Human c-I
35	198	51.3	604	2	AAW69295	Aaw69295 Human HIA
36	198	51.3	604	2	AAW52703	Aay52703 Human cel
37	198	51.3	604	2	AAW33997	Aay33997 Human cel
38	198	51.3	604	5	ABG65664	Abg65664 Human inh
39	198	51.3	604	6	ABU07431	Abu07431 Protein d
40	198	51.3	604	6	ABB82739	Abb82739 Human CIA
41	198	51.3	604	7	ADB80948	Adb80948 RING-SH c
42	198	51.3	604	7	AAE39811	Aae39811 Human cel
43	198	51.3	1140	5	AAU97837	Aau97837 Human cys
44	198	51.3	1141	4	AAW50694	Aab50694 Human API
45	189	49.0	600	2	AAW69298	Aaw69298 Murine HI

ALIGNMENTS

RESULT 1
AAW19584
ID AAW19584 standard; protein; 496 AA.
XX

AC AAW19584;

DT 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor M-XIAP.

DE Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis.

XX Mus sp.

OS Mus sp.

XX Key Location/Qualifiers

FT Domain 26..93

FT Domain /label= BIR-1

FT Domain 163..230

FT Domain /label= BIR-2

FT Domain 264..329

FT Domain /label= BIR-3

FT Domain 438..483

FT Domain /label= Ring_zinc_finger

XX WO9706255-A2

PD 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB001022.

XX 04-AUG-1995; 95US-00511485.

PR 22-DEC-1995; 95US-00576956.

XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;

XX WPI; 1997-154262/14.

DR N-PSDB; AAT70839.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease.

PS Claim 27; Page 79-80; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP) and which are characterised by the presence of a ring
CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The M-XIAP amino acid sequence
CC was deduced from the m-xiap gene (AAT70839) isolated from a mouse embryo
CC cDNA library. The IAP olypeptides can be expressed in host cells (in
CC vitro or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease

XX Sequence 496 AA;

Query Match 100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEDPWDQAKCY 60
Db 264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEDPWDQAKCY 323

QY 61 PGCKYL 66

Db 324 PGCKYL 329

RESULT 2

AAW69297
ID AAW69297 standard; protein; 496 AA.

XX AAW69297;

DT 13-NOV-1998 (first entry)

XX Murine XIAP protein.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.

XX Mus sp.

XX WO9835693-A2.

XX 20-AUG-1998.

PF 13-FEB-1998; 98WO-IB000781.

XX 13-FEB-1997; 97US-00800929.

XX (UYOT-) UNIV OTTAWA.

XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;

DR WPI; 1998-467164/40.

DR N-PSDB; AAV55041.

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.

XX Disclosure; Fig 4; 147pp; English.

XX This sequence is the murine XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,

CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors

XX Sequence 496 AA;

Query Match 100.0%; Score 386; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEDPWDQAKCY 60
Db 264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEDPWDQAKCY 323

QY 61 PGCKYL 66

Db 324 PGCKYL 329

RESULT 3

ABG65666
ID ABG65666 standard; protein; 496 AA.

XX ABG65666;

XX 26-AUG-2002 (first entry)

DE Mouse inhibitor of apoptosis, XIAP.

XX Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.

XX Mus sp.

XX WO200226968-A2.

XX 04-APR-2002.

PF 27-SEP-2001; 2001WO-CA001379.

XX 28-SEP-2000; 2000US-00672717.

XX (UYOT-) UNIV OTTAWA.

PA (AEGE-) AEGERA THERAPEUTICS INC.

XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

DR WPI; 2002-479562/51.

DR N-PSDB; ABK93872.

XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.

XX Example 12; Fig 4; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for

CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence
XX
SQ Sequence 496 AA;

Query Match 100.0%; Score 386; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQAKCY 60
DB 264 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQAKCY 323
QY 61 PGCKYL 66
DB 324 PGCKYL 329

RESULT 4
ADB61828
ID ADB61828 standard; protein; 66 AA.

AC ADB61828;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; cIAP2; cIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; BIR 3 domain; mouse; murine.

OS Mus sp.
XX
XX WO2003040172-A2.
PN
XX 15-MAY-2003.
PD
XX
XX 12-NOV-2002; 2002WO-CA001738.
PF
XX
XX 09-NOV-2001; 2001US-0332300P.
PR
XX 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Boudreault A, Korneluk RG, La Casse E, Liston P;
PI
XX WPI; 2003-513532/48.
DR
XX Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
XX Disclosure; Fig 1B; 53pp; English.

XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in

CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (cIAP2) and HIAP2 (cIAP1) all possess three BIR domains and a carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.

XX
SQ Sequence 66 AA;

Query Match 96.4%; Score 372; DB 7; Length 66;
Best Local Similarity 97.0%; Pred. No. 8.4e-39;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQAKCY 60
DB 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQAKCY 60
QY 61 PGCKYL 66
DB 61 PGCKYL 66

RESULT 5
ABP72157
ID ABP72157 standard; protein; 496 AA.

XX ABP72157;
AC ABP72157;
XX
DT 22-APR-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis protein MIAP3.
XX
KW Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.

XX
OS Mus sp.
XX
XX WO2003004606-A2.
PN
XX 16-JAN-2003.
PD
XX
XX 03-JUL-2002; 2002WO-US021002.
PF
XX
XX 03-JUL-2001; 2001US-00898158.
PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA
XX Troy CM, Shelanski ML;
PI
XX WPI; 2003-210351/20.
DR
XX N-PSDB; ABZ58102.

XX
PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
PT treating cancer, neurodegenerative disorder or cardiomyopathy.
XX
PS Disclosure; Fig 15A; 124pp; English.
XX
CC The present sequence is the protein sequence of murine inhibitor of
CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as

CC an antisense oligonucleotide, which specifically hybridises to a nucleic
CC acid encoding an inhibitor of apoptosis protein, especially XIAP1, XIAP2,
CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
CC death comprises contacting the cell with the nucleic acid under
CC conditions permitting the nucleic acid to enter the cell, especially the
CC use of a vector, liposome, or a mechanical or electrical means. The
CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
CC cell carcinoma and squamous cell carcinoma (all claimed)
XX
SQ Sequence 496 AA;

Query Match 96.4%; Score 372; DB 6; Length 496;
Best Local Similarity 97.0%; Pred. No. 8.8e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 264 YEARIVTFTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 6
ADB61827
ID ADB61827 standard; protein; 66 AA.

XX ADB61827;
XX
DT 04-DEC-2003 (first entry)
XX
DE Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; BIR 3 domain; rat.

XX Rattus sp.
XX
PN WO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
PR 08-APR-2002; 2002US-0370934P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Boudreault A, Korneluk RG, La Casse E, Liston P;
XX
DR WPI; 2003-513532/48.

XX Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.

XX This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat

CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus). The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and a carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.

XX
SQ Sequence 66 AA;

Query Match 94.8%; Score 366; DB 7; Length 66;
Best Local Similarity 93.9%; Pred. No. 4.7e-38;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIVTFTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 1 YDARIVTFTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWEQHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 7
ADB61810
ID ADB61810 standard; protein; 66 AA.

XX ADB61810;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; human; BIR 3 domain.

XX Homo sapiens.

XX WO2003040172-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-CA001738.

XX 09-NOV-2001; 2001US-0332300P.

PR 08-APR-2002; 2002US-0370934P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Boudreault A, Korneluk RG, La Casse E, Liston P;

XX

DR WPI; 2003-513532/48.
XX Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1A; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention
CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC against which the peptides of the invention are targeted to bind.
XX
SQ Sequence 66 AA;

Query Match 94.8%; Score 366; DB 7; Length 66;
Best Local Similarity 95.5%; Pred. No. 4.7e-38;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 8
ABG32418
ID ABG32418 standard; protein; 236 AA.
XX
AC ABG32418;
DT 15-NOV-2002 (first entry)
XX
DE X-linked inhibitor of apoptosis protein, XIAP.
XX Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
KW fertility; testicular cancer; male infertility; male birth control;
KW X-linked inhibitor of apoptosis protein; XIAP.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by nnn; start codon is illegible in
FT specification"
FT
XX US2002086409-A1.
XX
PD 04-JUL-2002.
XX
PF 18-DEC-2001; 2001US-00024433.

XX 29-JAN-1998; 98US-0073001P.
PR 29-JAN-1999; 99US-00239867.
XX
PA (KORN/) KORNELUK R G.
PA (LAGA/) LAGACE M.
XX
PI Korneluk RG, Lagace M;
XX
DR WPI; 2002-642245/69.
DR N-PSDB; ABS52803.
XX
PT Novel polypeptide, a member of inhibitor of apoptosis family of proteins
PT that is expressed in testes useful for modulating apoptosis in cells,
PT particular cells involved in male fertility.
XX
PS Example 3; Fig 4B; 24pp; English.
XX
CC A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (I) is
CC useful for identifying a compound that modulates TIAP biological activity
CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (I) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. TIAP may be manipulated for use as a male
CC birth control. TIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the amino
CC acid sequence of X-linked inhibitor of apoptosis protein, XIAP
XX
SQ Sequence 236 AA;

Query Match 94.8%; Score 366; DB 5; Length 236;
Best Local Similarity 95.5%; Pred. No. 2.1e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 4 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 9
AAO20511
ID AAO20511 standard; protein; 278 AA.
XX
AC AAO20511;
DT 27-JUN-2002 (first entry)
XX
DE Protein of APP related human homologue hCP35211.
XX
KW Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP011345.
XX
PR 29-SEP-2000; 2000US-0236893P.
PR 14-JUN-2001; 2001US-0298309P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX

PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWHM, Zusman S;
XX
DR WPI; 2002-315796/35.
DR N-PSDB; AAK99405.
XX
XX New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease.
XX
XX Example 4; Page 112; 129pp; English.
XX
XX The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This sequence represents the
CC protein of the APP related human homologue hCP35211
XX
SQ Sequence 278 AA;
Query Match 94.8%; Score 366; DB 5; Length 278;
Best Local Similarity 95.5%; Pred. No. 2.5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWDQHAKCY 60
Db 46 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 105
QY 61 PGCKYL 66
Db 106 PGCKYL 111
RESULT 10
AAW19581
ID AAW19581 standard; protein; 497 AA.
XX
AC AAW19581;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor XIAP.
XX
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 26..93
FT /label= BIR-1
FT Domain 163..230
FT /label= BIR-2
FT Domain 265..330
FT /label= BIR-3
FT Domain 439..484
FT /label= Ring_zinc_finger
XX
XX WO9706255-A2.
PN
XX
PD 20-FEB-1997.
XX

PF 05-AUG-1996; 96WO-IB001022.
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
PA (UYOT-) UNIV OTTAWA.
XX
XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
PI
XX WPI; 1997-154262/14.
DR N-PSDB; AAT70836.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
PS Claim 27; Page 68-70; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP) and which are characterised by the presence of a ring
CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
CC or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease
XX
SQ Sequence 497 AA;
Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWDQHAKCY 60
Db 265 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 11
AAW69294
ID AAW69294 standard; protein; 497 AA.
XX
AC AAW69294;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human XIAP protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein.
XX
OS Homo sapiens.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
XX

DR WPI; 1998-467164/40.
DR N-PSDB; AAV55038.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Disclosure; Fig 1; 147pp; English.
XX
CC This sequence is the human XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 60
Db |||||
265 YEARIFTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWEQHAKWY 324
|||
QY 61 PGCKYL 66
Db |||||
325 PGCKYL 330

RESULT 12
AAV59451
ID AAY59451 standard; protein; 497 AA.
XX
AC AAY59451;
XX
DT 24-MAR-2000 (first entry)
XX
DE Human XIAP protein sequence.
XX
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta.
XX
OS Homo sapiens.
XX
PN JP11326328-A.
XX
PD 26-NOV-1999.
XX
PF 13-MAY-1998; 98JP-00130378.
XX
PR 13-MAY-1998; 98JP-00130378.
XX
PA (MATS/) MATSUMOTO K.
XX
DR WPI; 2000-078337/07.
DR N-PSDB; AAZ48862.
XX
PT Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein.

XX
PS Claim 3; Page 28-30; 43pp; Japanese.
XX
CC This sequence represents the human XIAP protein. The invention relates to
CC a method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1(TAK1) binding
CC protein 1(TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (Transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug
XX
SQ Sequence 497 AA;

Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWDQHAKCY 60
Db |||||
265 YEARIFTFTGWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWEQHAKWY 324
|||
QY 61 PGCKYL 66
Db |||||
325 PGCKYL 330

RESULT 13
AAV99985
ID AAY99985 standard; protein; 497 AA.
XX
AC AAY99985;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human X-linked inhibitor of apoptosis.
XX
KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
KW antiinflammatory; cytostatic; tumour.
XX
OS Homo sapiens.
XX
PN US6087173-A.
XX
PD 11-JUL-2000.
XX
PF 09-SEP-1999; 99US-00392580.
XX
PR 09-SEP-1999; 99US-00392580.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM, Ackermann EJ;
XX
DR WPI; 2000-498201/44.
DR N-PSDB; AAA64901.
XX
PT Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
XX
PS Example 13; Col 43-48; 33pp; English.
XX
CC The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis (the
CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
CC more effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis

CC expression in cells and tissues in vitro. The oligonucleotides are also
CC useful for treating animals or humans, prone to a disease associated with
CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
CC prophylactically to prevent infection, inflammation or tumour formation
XX
SQ Sequence 497 AA;
Query Match 94.8%; Score 366; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 265 YEARIIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 14
ABG65663
ID ABG65663 standard; protein; 497 AA.
XX
AC ABG65663;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human inhibitor of apoptosis, XIAP.
XX
KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX
OS Homo sapiens.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI; 2002-479562/51.
DR N-PSDB; ABK93869.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 1; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,

CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence
XX
SQ Sequence 497 AA;
Query Match 94.8%; Score 366; DB 5; Length 497;
Best Local Similarity 95.5%; Pred. No. 5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEARIIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
Db 265 YEARIIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKCY 60
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 15
ADB80961
ID ADB80961 standard; protein; 497 AA.
XX
AC ADB80961;
XX
DT 04-DEC-2003 (first entry)
XX
DE RING-SH complex related protein, SEQ ID No 35.
XX
KW RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KW Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsg101;
KW cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KW rhabdovirus; filovirus.
XX
OS Unidentified.
XX
PN WO2003033646-A2.
XX
PD 24-APR-2003.
XX
PF 31-JUL-2002; 2002WO-US024589.
XX
PR 31-JUL-2001; 2001US-0308958P.
PR 09-NOV-2001; 2001US-0345846P.
XX
PA (PROT-) PROTEOLOGICS INC.
XX
PI Greener T, Moskowitz H, Reiss Y, Alroy I;
XX
DR WPI; 2003-393509/37.
DR N-PSDB; ADB81002.
XX
PT New isolated protein complex comprising a RING-SH 3 polypeptide and
PT another polypeptide, useful for detecting cells infected with a virus,
PT and for treating viral disorders caused by retroviruses, rhabdoviruses,
PT or filoviruses.
XX
PS Disclosure; Fig 35; 176pp; English.
XX
CC The invention relates to a novel isolated protein complex comprising a
CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
CC STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a
CC clathrin. The novel protein complex has virucide activity and can be used
CC to treat disorders as part of a vaccine. The protein complex and
CC composition are useful for detecting cells infected with a virus, for
CC identifying agents having antiviral activity, and for treating viral
CC disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
CC sequence is a protein comprising the RING-SH complex of the invention.
XX

Search completed: March 10, 2004, 13:52:28
Job time : 51.5 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:52:35 ; Search time 29 Seconds
(without alignments)
480.556 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	386	100.0	66	9 US-09-201-936-24	Sequence 24, Appl
2	386	100.0	496	9 US-09-974-592-10	Sequence 10, Appl
3	386	100.0	496	9 US-09-201-936-10	Sequence 10, Appl
4	366	94.8	66	9 US-09-201-936-25	Sequence 25, Appl
5	366	94.8	107	9 US-09-965-967-20	Sequence 20, Appl
6	366	94.8	278	9 US-09-964-899-39	Sequence 39, Appl
7	366	94.8	497	9 US-09-974-592-4	Sequence 4, Appl
8	366	94.8	497	9 US-09-201-936-4	Sequence 4, Appl
9	233	60.4	50	14 US-10-138-618-28	Sequence 28, Appl
10	233	60.4	50	14 US-10-138-618-29	Sequence 29, Appl
11	233	60.4	50	14 US-10-138-618-32	Sequence 32, Appl
12	198	51.3	68	9 US-09-201-936-26	Sequence 26, Appl
13	198	51.3	604	9 US-09-974-592-6	Sequence 6, Appl
14	198	51.3	604	9 US-09-201-936-6	Sequence 6, Appl
15	198	51.3	604	14 US-10-232-286-4	Sequence 4, Appl

16	198	51.3	604	14	US-10-141-618-6	Sequence 6, Appl
17	198	51.3	1140	14	US-10-353-461-8	Sequence 8, Appl
18	190	49.2	68	9	US-09-201-936-28	Sequence 28, Appl
19	190	49.2	68	14	US-10-041-859-18	Sequence 18, Appl
20	190	49.2	172	14	US-10-041-859-12	Sequence 12, Appl
21	190	49.2	268	14	US-10-323-643-10	Sequence 10, Appl
22	189	49.0	600	9	US-09-974-592-12	Sequence 12, Appl
23	185	47.9	68	14	US-10-041-859-14	Sequence 14, Appl
24	185	47.9	172	14	US-10-041-859-8	Sequence 8, Appl
25	185	47.9	346	14	US-10-041-859-2	Sequence 2, Appl
26	184	47.7	68	9	US-09-201-936-27	Sequence 27, Appl
27	184	47.7	612	9	US-09-974-592-14	Sequence 14, Appl
28	184	47.7	612	14	US-10-232-286-14	Sequence 14, Appl
29	184	47.7	618	9	US-09-974-592-8	Sequence 8, Appl
30	184	47.7	618	9	US-09-201-936-8	Sequence 8, Appl
31	183	47.4	438	8	US-08-464-588-2	Sequence 2, Appl
32	183	47.4	438	14	US-10-323-643-2	Sequence 2, Appl
33	183	47.4	602	9	US-09-201-936-40	Sequence 40, Appl
34	183	47.4	618	14	US-10-153-668-338	Sequence 338, App
35	183	47.4	618	14	US-10-207-655-200	Sequence 200, App
36	183	47.4	618	14	US-10-232-286-2	Sequence 2, Appl
37	178	46.1	68	14	US-10-041-859-19	Sequence 19, Appl
38	178	46.1	109	9	US-09-965-967-30	Sequence 30, Appl
39	178	46.1	172	14	US-10-041-859-13	Sequence 13, Appl
40	178	46.1	591	9	US-09-201-936-42	Sequence 42, Appl
41	177	45.9	68	14	US-10-041-859-16	Sequence 16, Appl
42	177	45.9	172	14	US-10-041-859-10	Sequence 10, Appl
43	177	45.9	280	14	US-10-244-586-3	Sequence 3, Appl
44	177	45.9	298	14	US-10-235-026-2	Sequence 2, Appl
45	177	45.9	355	14	US-10-203-708-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match 100.0%; Score 386; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.4e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60

Db 1 YEARIVFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWDQAKCY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2

US-09-974-592-10
; Sequence 10, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10

Query Match 100.0%; Score 386; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAKCY 60
Db 264 YEARIVTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3

US-09-201-936-10
; Sequence 10, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match 100.0%; Score 386; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIVTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAKCY 60
Db 264 YEARIVTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4

US-09-201-936-25
; Sequence 25, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 94.8%; Score 366; DB 9; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.3e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWDQHAKCY 60
Db 1 YEARIFTFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDMKPSDPPWEQHAKWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 5

US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830

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; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

Query Match          94.8%; Score 366; DB 9; Length 107;
Best Local Similarity 95.5%; Pred. No. 2.2e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 15 YEARIFTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 74

QY 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 6
US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

Query Match          94.8%; Score 366; DB 9; Length 278;
Best Local Similarity 95.5%; Pred. No. 6.1e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 46 YEARIFTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 105

QY 61 PGCKYL 66
Db 106 PGCKYL 111

RESULT 7
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
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; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match          94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.1e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 265 YEARIFTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 8
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match          94.8%; Score 366; DB 9; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.1e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 265 YEARIFTGTTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 9
US-10-138-618-28
; Sequence 28, Application US/10138618
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;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match      60.4%; Score 233; DB 14; Length 50;
Best Local Similarity 95.0%; Pred. No. 2.3e-21;
Matches 38; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALGEGDKVKCFHCGGLTDWKPSDDPDQHAKCYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGLTDWKPSDDPDQHAKCYPGCKYL 40

RESULT 12
US-09-201-936-26
; Sequence 26, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26

Query Match      51.3%; Score 198; DB 9; Length 68;
Best Local Similarity 55.9%; Pred. No. 6.7e-17;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFTGIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58
Db 1 HAARFKTFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPDWVQHAK 60

Qy 59 CYPGCKYL 66
Db 61 WFPRC EYL 68

US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
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; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6

Query Match      51.3%; Score 198; DB 9; Length 604;
Best Local Similarity 55.9%; Pred. No. 7.1e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFTGIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58
Db 255 HAARFKTFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPDWVQHAK 314

Qy 59 CYPGCKYL 66
Db 315 WFPRC EYL 322

RESULT 14
US-09-201-936-6
; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-6

Query Match      51.3%; Score 198; DB 9; Length 604;
Best Local Similarity 55.9%; Pred. No. 7.1e-16;
Matches 38; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 1 YEARIVTFTGIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58
Db 255 HAARFKTFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPDWVQHAK 314

Qy 59 CYPGCKYL 66
Db 315 WFPRC EYL 322

RESULT 15
US-10-232-286-4
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Search completed: March 10, 2004, 13:56:59
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:49:29 ; Search time 13 Seconds
(without alignments)
488.357 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIVTFTGIYSVNKEQL.....KPSDEPDWDQHAQKYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	366	94.8	497	2 S69544	apoptosis inhibito
2	198	51.3	604	2 S68449	apoptosis inhibito
3	196	50.8	358	2 JC5964	apoptosis inhibito
4	190	49.2	268	2 T10304	inhibitor of apopt
5	190	49.2	268	2 A53989	apoptosis-inhibiti
6	184	47.7	618	2 S68450	apoptosis inhibito
7	177	45.9	298	2 JC7568	kidney inhibitor o
8	175	45.3	275	2 A45679	inhibitor-of-apopt
9	164.5	42.6	1232	2 A55478	neuronal apoptosis
10	160.5	41.6	1447	2 T42628	apoptosis inhibito
11	149	38.6	496	2 S68452	apoptosis inhibito
12	149	38.6	497	2 S69545	apoptosis inhibito
13	141	36.5	208	2 T03183	probable apoptosis
14	128	33.2	275	2 T10310	apoptosis-inhibiti
15	126	32.6	150	2 T28409	ORF MSV248 probabl
16	114.5	29.7	4845	2 T31067	BIR repeat contain
17	108	28.0	286	2 D36828	orf13 protein - Au
18	106	27.5	292	2 T41772	IAP1 orf27 - Bomby
19	100	25.9	155	2 T37471	apoptosis inhibito
20	99	25.6	155	2 T30489	apoptosis inhibito
21	93	24.1	308	2 T37474	apoptosis inhibito
22	84.5	21.9	997	2 T43523	cut17 protein - fi
23	83.5	21.6	329	2 T28403	ORF MSV242 probabl
24	80.5	20.9	564	2 C42523	A55R protein - vac
25	80.5	20.9	564	2 JQ1792	SalF17R protein -
26	66.5	17.2	187	2 T50621	hypothetical prote
27	66	17.1	511	2 T43634	nicotinic acetylch
28	66	17.1	534	2 T25720	hypothetical prote
29	65.5	17.0	737	2 PQ0219	RNA-2 polypeptide

30	65	16.8	466	2 PC4296	nicotinic acetylch
31	64.5	16.7	324	2 S39502	vegetative storage
32	64.5	16.7	506	2 S13720	coat protein - ara
33	64	16.6	204	2 H70609	probable dna-3-met
34	63	16.3	249	2 H72858	apoptosis inhibito
35	62.5	16.2	336	2 H81785	conserved hypothet
36	61.5	15.9	336	2 B81210	conserved hypothet
37	61.5	15.9	1808	2 T15099	hypothetical prote
38	60.5	15.7	437	2 AG0766	probable dehydrata
39	60.5	15.7	788	2 S70079	1,4-alpha-glucan b
40	60.5	15.7	1798	2 S53869	laminin beta-2 cha
41	60	15.5	246	2 I50127	MHC class II histo
42	60	15.5	249	2 T41814	IAP2 orf71 - Bomby
43	60	15.5	252	2 I50126	MHC class II histo
44	59.5	15.4	459	2 S76138	hypothetical prote
45	59.5	15.4	607	2 T39823	hypothetical prote

ALIGNMENTS

RESULT 1

S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, N
EMBO J. 15, 2685-2694, 1996
A>Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32974; NID:gl016687; PIDN:AAC50518.1; PID:gl016688
R>Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahar
Nature 379, 349-353, 1996
A>Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of 1
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161,'C',163-422,'Q',424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:gl184319; PIDN:AAC50373.1; PID:gl184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 94.8%; Score 366; DB 2; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.2e-33;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDWDQHAQKY 60
Db 265 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDEPDWEQHAQWY 324

Qy 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 2

S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R>Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahan

A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DBSJ
A;Molecule type: DNA
A;Residues: 1-268 <AHR>
A;Cross-references: EMBL:U75930: NID:α2934903: PIDN:AAC59034.1: PID:q1911281

Query Match 47.7%; Score 184; DB 2; Length 618;
Best Local Similarity 51.5%; Pred. NO. 5.6e-13;
Matches 35; Conservative 9; Mismatches 22; Indels

Search completed: March 10, 2004, 13:55:04
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:54 ; Search time 10.5 Seconds
(without alignments)
327.298 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIVTGTWISYVNKEQL.....KPSDEPMDQHAKYCPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 141681
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	94.8	496	1 BIR4 RAT	Q9r0i6 rattus norv
2	366	94.8	497	1 BIR4_HUMAN	P98170 homo sapien
3	357	92.5	496	1 BIR4_MOUSE	Q60989 mus musculu
4	334	86.5	236	1 BIR8_HUMAN	Q96p09 homo sapien
5	328	85.0	236	1 BIR8_PANTR	Q95m72 pan troglod
6	325	84.2	236	1 BIR8_GORGO	Q95m71 gorilla gor
7	198	51.3	604	1 BIR3_HUMAN	Q13489 homo sapien
8	196	50.8	358	1 PIAP_PIG	Q62640 sus scrofa
9	192	49.7	611	1 BIR_CHICK	Q90660 gallus gall
10	190	49.2	268	1 IAP3_NPVOP	P41437 orgyia pseu
11	189	49.0	600	1 BIR3_MOUSE	Q08863 mus musculu
12	184	47.7	612	1 BIR2_MOUSE	Q62210 mus musculu
13	183	47.4	618	1 BIR2_HUMAN	Q13490 homo sapien
14	178	46.1	438	1 IAP1_DROME	Q24306 drosophila
15	177	45.9	298	1 BIR7_HUMAN	Q96ca5 homo sapien
16	175	45.3	275	1 IAP_GVCP	P41436 cydia pomon
17	164.5	42.6	1403	1 BIR1_HUMAN	Q13075 homo sapien
18	164.5	42.6	1403	1 BIRF_MOUSE	Q9jib6 mus musculu
19	163.5	42.4	1402	1 BIRG_MOUSE	Q9jib3 mus musculu
20	163.5	42.4	1403	1 BIRA_MOUSE	Q9qwk5 mus musculu
21	163.5	42.4	1403	1 BIRE_MOUSE	Q9r016 mus musculu
22	160.5	41.6	1447	1 BIRB_MOUSE	Q9qk4 mus musculu
23	149	38.6	498	1 IAP2_DROME	Q24307 drosophila
24	141	36.5	208	1 ZFP_IRV6	P47732 chilo iride
25	128	33.2	275	1 IAP1_NPVOP	Q10296 orgyia pseu
26	121.5	31.5	142	1 BIR5_RAT	Q9jhy7 rattus norv
27	119.5	31.0	140	1 BIR5_MOUSE	O70201 mus musculu
28	114.5	29.7	142	1 BIR5_HUMAN	O15392 homo sapien
29	114.5	29.7	4829	1 BIR6_HUMAN	Q9nr09 homo sapien
30	108	28.0	286	1 IAP1_NPVAC	P41435 autographa
31	84.5	21.9	997	1 BIR1_SCHPO	O14064 schizosacch
32	80.5	20.9	564	1 VA55_VACCC	P21073 vaccinia vi
33	80.5	20.9	564	1 VA55_VACCV	P24768 vaccinia vi

34	66	17.1	511	1 ACH5 CAEEL	Q23022 caenorhabdi
35	64.5	16.7	506	1 POL2_ARMV	P24819 arabis mosa
36	63	16.3	249	1 IAP2_NPVAC	P41454 autographa
37	61.5	15.9	436	1 ACHX_ONCVO	P54247 onchocerca
38	61	15.8	198	1 RK24_ARATH	P92959 arabidopsi
39	60.5	15.7	589	1 AXU1_HUMAN	Q96s65 homo sapien
40	60.5	15.7	774	1 GLB1_STRCO	Q59833 streptomyc
41	60.5	15.7	1798	1 LMB2_HUMAN	P55268 homo sapien
42	59.5	15.4	512	1 GATA_BORBR	O7wev1 bordetella
43	59.5	15.4	512	1 GATA_BORPA	Q7w3h7 bordetella
44	59.5	15.4	512	1 GATA_BORPE	O7vsn2 bordetella
45	59.5	15.4	607	1 PESC_SCHPO	O60164 schizosacch

ALIGNMENTS

RESULT 1
BIR4_RAT
ID BIR4 RAT STANDARD; PRT; 496 AA.
AC Q9R0I6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIRC4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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EMBL; AB033366; BA85304.1; --
HSSP; Q13490; IQEH.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
SMART; SM00238; BIR; 3.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS0089; ZF_RING_2; 1.
Apoptosis; Zinc-finger; Repeat.
REPEAT 26 93 BIR 1.
REPEAT 163 230 BIR 2.
REPEAT 264 329 BIR 3.
FT

FT ZN FING 449 484 RING-TYPE.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 94.8%; Score 366; DB 1; Length 496;
Best Local Similarity 93.9%; Pred. No. 3.4e-36;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIVFTGTWISYNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHAQCY 60
Db 264 YDARIVFTGTWISYNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPMDQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
BIR4 HUMAN STANDARD; PRT; 497 AA.
ID_BIR4 HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9NQ14;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP-like protein) (HILP).
GN BIRC4 OR API3 OR IAP3 OR XIAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:349-353 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA Gilfillan M.C., Shields H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors."
RL EMBO J. 15:2685-2694 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442;
RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases."
RL Nature 388:300-304 (1997).
RN [6]
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "HtrA2 promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins."
RL J. Biol. Chem. 277:445-454 (2002).
RN [7]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637;
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
RA Herrmann J., Wu J.C., Fesik S.W.;
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
RT domain."
RL Nature 408:1004-1008 (2000).
CC -I- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
CC -I- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -I- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains.
CC -I- SIMILARITY: Belongs to the IAP family.
CC -I- SIMILARITY: Contains 3 BIR repeats.
CC -I- SIMILARITY: Contains 1 RING-type zinc finger.

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CC or send an email to license@isb-sib.ch).

CC EMBL; U45880; AAC50373.1; -.
CC EMBL; U32974; AAC50518.1; -.
CC EMBL; AL121601; CAB95312.1; -.
CC EMBL; BC032729; AAH32729.1; -.
CC PIR; S69544; S69544.
CC PDB; 1G3F; 10-JAN-01.
CC PDB; 1C9Q; 09-AUG-00.
CC PDB; 1F9X; 11-JUL-01.
CC PDB; 1G73; 10-JAN-01.
CC PDB; 1I30; 26-SEP-01.
CC PDB; 1I40; 31-OCT-01.
CC PDB; 1I51; 23-FEB-02.
CC PDB; 1KMC; 16-JAN-02.
CC Genew; HGNC:592; BIRC4.
CC MIM; 300079; -.
CC GO; GO:0005829; C:cytosol; TAS.
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.

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DR PROSITE; PS00143; BIR_REPEAT 2; 3.
DR PROSITE; PS00518; ZF_RING 1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING 2; 1.
KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT MUTAGEN 214 214 D->S: REDUCED INTERACTION WITH PRSS25.
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND WITH PRSS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 Q -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394CI6D45EB635 CRC64;

Query Match 94.8%; Score 366; DB 1; Length 497;
Best Local Similarity 95.5%; Pred. No. 3.4e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIVTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQAKCY 60
Db 265 YEARIFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQAKCY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 3
BIR4_MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60989; O08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP homolog A) (MIAP3) (MIAP-3).
DE BIRC4 OR API3 OR XIAP OR AIPA OR MIHA.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
-----
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CC -----
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB59376.1; -.
DR HSSP; Q13490; IQBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT 1; 3.
DR PROSITE; PS0143; BIR_REPEAT 2; 3.
DR PROSITE; PS00518; ZF_RING 1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING 2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

Query Match 92.5%; Score 357; DB 1; Length 496;
Best Local Similarity 93.9%; Pred. No. 4e-35;
Matches 62; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIVTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQAKCY 60
Db 264 YEARIVTGWTSSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQAKCY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
BIR8_HUMAN
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific inhibitor of apoptosis).
DE BIRC8 OR ILP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J., Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
```


CC similarity).

CC -!- SUBUNIT: Binds to caspase-9 (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 1 BIR repeat.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AY030053; AAK49777.1; -.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 1.

DR SMART; SM00238; BIR; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.

DR PROSITE; PS0143; BIR_REPEAT_2; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Apoptosis; Zinc-finger.

FT REPEAT 7 70 BIR.

FT ZN_FING 189 224 RING-TYPE.

SQ SEQUENCE 236 AA; 27120 MW; C3A70E39EBE42E4C CRC64;

Query Match 84.2%; Score 325; DB 1; Length 236;

Best Local Similarity 78.8%; Pred. No. 1.3e-31;

Matches 52; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARIVTFTWYISVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWOHAKCY 60

DB 4 YEAWLITFTWYISVNKEQLARAGFYAIGQEDKIQCFCGGLANWKPEDPWEQAKWY 63

QY 61 PGCKYL 66

DB 64 PGCKYL 69

RESULT 7

BIR3_HUMAN STANDARD; PRT; 604 AA.

ID BIR3_HUMAN

AC Q13489; Q16628; Q9HC27; Q9UP46;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis

DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex

DE protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (API2).

GN BIRC3 OR API2 OR IAP1 OR MIHC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96128127; PubMed=8548810;

RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;

RT "The TNFR2-TRAF signaling complex contains two novel proteins related

RT to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96149249; PubMed=8552191;

RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,

RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;

RT "Suppression of apoptosis in mammalian cells by NAIP and a related

RT family of IAP genes.";

RL Nature 379:349-353(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=96209843; PubMed=8643514;

RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;

RT "Cloning and expression of apoptosis inhibitory protein homologs that

RT function to inhibit apoptosis and/or bind tumor necrosis factor

RT receptor-associated factors.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=99252096; PubMed=10233894;

RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,

RA ten Cate J.W., Pannekoek H.;

RT "Vascular endothelial genes that are responsive to tumor necrosis

RT factor-alpha in vitro are expressed in atherosclerotic lesions,

RT including inhibitor of apoptosis protein-1, stannin, and two novel

RT genes.";

RL Blood 93:3418-3431(1999).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [6]

RP SEQUENCE OF 362-441 FROM N.A.

RX MEDLINE=20519161; PubMed=11066071;

RA Baens M., Steyls A., Dierlam J., De Wolf-Peeters C., Marynen P.;

RT "Structure of the MLT gene and molecular characterization of the

RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone

RT B-cell lymphomas of MALT type.";

RL Genes Chromosomes Cancer 29:281-291(2000).

CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS

CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions

CC inhibit apoptotic suppressor activity.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN

CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,

CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.

CC -!- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation

CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid

CC tissue). This translocation is found in approximately 50% of

CC cytogenetically abnormal low-grade MALT lymphoma and involves

CC MALT1 and BIRC3.

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

CC WWW="http://www.infobiogen.fr/services/chronocancer/BIRC3ID239.html".

CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L49433; AAC42078.1; -
CC EMBL: U88909; AAC53532.1; -
CC HSP: Q13490; IQBH.
CC MGD; MGI:1197009; Birc3.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS01143; BIR_REPEAT_2; 3.
CC PROSITE; PS0209; CARD; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 47.7%; Score 184; DB 1; Length 612;
Best Local Similarity 51.5%; Pred. No. 2.4e-14;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPPDQHAH 58
Db 262 HSARLRTFLYWPSPVPQPEQLASAGFYVDRNDVVKCFCCDGLRCWEPGDDPWIEHAK 321

QY 59 CYPGCKYL 66
Db 322 WFPRCEFL 329

RESULT 13
BIR2_HUMAN STANDARD; PRT; 618 AA.
AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC2 OR API1 OR IAP2 OR MIH8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
to baculoviral inhibitor of apoptosis proteins."

RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE=99332054; PubMed=10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC EMBL; L49431; AAC41942.1; -
DR EMBL; U45879; AAC50372.1; -
DR EMBL; U37547; AAC50508.1; -
DR EMBL; BC016174; AAH16174.1; -
DR EMBL; BC028578; AAH28578.1; -
DR PIR; S68450; S68450.
DR PDB; IQBH; 20-OCT-99.
DR Genew; HGNC:590; BIRC2.
DR MIM; 601712; -.
DR GO; GO:0008189; P:apoptosis inhibitor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
KW REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 543 CARD.
FT ZN_FING 571 606 RING-TYPE.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
FT TURN 269 270
FT HELIX 271 274
FT HELIX 287 293
FT TURN 294 294
FT TURN 296 297
FT TURN 301 304
FT STRAND 309 309
FT HELIX 322 325
FT TURN 326 328
FT STRAND 333 333
FT TURN 334 343
FT HELIX 344 351
FT TURN 353 354
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 47.4%; Score 183; DB 1; Length 618;
Best Local Similarity 51.5%; Pred. No. 3.1e-14;
Matches 35; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58
Db 269 HAARMRTFWYWPSSVPVQPEQLASAGFYVGRNDDVKCFCCDGLRCWESGDDPDVWEHAK 328

QY 59 CYPGCKYL 66
Db 329 WFPRCFEL 336

RESULT 14
IAP1_DROME
ID IAP1_DROME STANDARD; PRT; 438 AA.
AC Q24306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (diap1) (Thread protein).
```

```
GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye imaginal disk;
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A., Wassarman D.A., Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RT function to block cell death.";
RL Cell 83:1253-1262(1995).
CC -|- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC -|- HID-DEPENDENT CELL DEATH IN THE EYE.
CC -|- SIMILARITY: Belongs to the IAP family.
CC -|- SIMILARITY: Contains 2 BIR repeats.
CC -|- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L49440; AAC41609.1; -.
DR PDB; 1JD4; 05-DEC-01.
DR PDB; 1JD5; 05-DEC-01.
DR PDB; 1JD6; 05-DEC-01.
DR FlyBase; FBgn0003691; th.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 44 110 BIR 1.
FT REPEAT 226 293 BIR 2.
FT ZN_FING 391 426 RING-TYPE.
SQ SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;

Query Match 46.1%; Score 178; DB 1; Length 438;
Best Local Similarity 45.5%; Pred. No. 8.8e-14;
Matches 30; Conservative 15; Mismatches 19; Indels 2; Gaps 1;

QY 3 ARIVTFGTWIYSVNKE--QLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAKCY 60
Db 228 ARLRTFEAWPRNLKQKPHQLAEAGFFYTGVDVRVRCFSCGGGLMDWNDNDEPWEQHALWL 287

QY 61 PGCKYL 66
Db 288 SQCRFV 293

RESULT 15
BIR7_HUMAN
ID BIR7_HUMAN STANDARD; PRT; 298 AA.
AC Q96CA5; Q9BQV0; Q9H2A8; Q9HAP7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of
DE apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
```

DE (ML-IAP) (Livin).
GN BIRC7 OR KIAP OR MLIAP OR LIVIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal kidney;
RX MEDLINE=21092523; PubMed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "KIAP, a novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX MEDLINE=21223043; PubMed=11322947;
RA Ashhab Y., Alian A., Polliack A., Panet A., Yehuda D.B.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
different biological properties and tissue distribution pattern.";
RL FEBS Lett. 495:56-60(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX PubMed=11024045;
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis protein family member.";
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND
ASP-138.
RX MEDLINE=20538921; PubMed=11084335;
RA Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
RT "ML-IAP, a novel inhibitor of apoptosis that is preferentially
expressed in human melanomas.";
RL Curr. Biol. 10:1359-1366(2000).
RN [7]
RP INTERACTION WITH SMAC.
RX MEDLINE=21922807; PubMed=11801603;
RA Vucic D., Deshayes K., Ackerly H., Pisabarro M.T., Kadkhodayan S.,
RA Fairbrother W.J., Dixit V.M.;
RT "SMAC negatively regulates the anti-apoptotic activity of melanoma
inhibitor of apoptosis (ML-IAP).";
RL J. Biol. Chem. 277:12275-12279(2002).
RN [8]
RP ACTIVATION OF MAP KINASES.
RX MEDLINE=21853687; PubMed=11865055;
RA Sanna M.G., da Silva Correia J., Ducrey O., Lee J., Nomoto K.,
RA Schrantz N., Deveraux Q.L., Ulevitch R.J.;
RT "IAP suppression of apoptosis involves distinct mechanisms: the
TAK1/JNK1 signaling cascade and caspase inhibition.";
RL Mol. Cell. Biol. 22:1754-1766(2002).
CC -!- FUNCTION: Protects against apoptosis induced by TNF or by chemical
agents such as adriamycin, etoposide or staurosporine. Suppression
of apoptosis is mediated by activation of MAPK8/JNK1, and possibly
also of MAPK9/JNK2. This activation depends on TAB1 and
NR2C2/TAK1. In vitro, inhibits caspase-3 and proteolytic
activation of pro-caspase-9. Isoform 1 blocks staurosporine-
induced apoptosis and isoform 2 blocks etoposide-induced
apoptosis.
CC -!- SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR
domain disrupts binding to caspase-9 and apoptotic suppressor
activity. Interacts with TAB1. In vitro, interacts with caspase-3
and caspase-7 via its BIR domain.
CC -!- SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern
throughout the cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=2; Synonyms=Livin alpha;
IsoId=Q96CA5-1; Sequence=Displayed;
Name=1; Synonyms=Livin beta;
IsoId=Q96CA5-2; Sequence=VSP_002459;
Name=3;
IsoId=Q96CA5-3; Sequence=VSP_002458;
CC -!- TISSUE SPECIFICITY: Very low levels or not detectable in most
adult tissues. Detected in adult heart, placenta, lung, lymph
node, spleen and ovary, and in several carcinoma cell lines
(isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in
fetal kidney, heart and spleen, and at lower levels in adult
brain, skeletal muscle and peripheral blood leukocytes.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch.
CC -----

DR EMBL; AF301009; AAG37878.1; -
DR EMBL; AJ309298; CAC37337.1; -
DR EMBL; AJ309298; CAC37338.1; -
DR EMBL; AF311388; AAG33622.1; -
DR EMBL; AL121827; CAC36111.1; -
DR EMBL; AL121827; CAC36112.1; -
DR EMBL; AL121827; CAC36113.1; ALT_INIT.
DR EMBL; BC014475; AAHL4475.1; -
DR PIR; JC7568; JC7568.
DR HSSP; Q13490; IQBH.
DR Genew; HGNC:13702; BIRC7.
DR MIM; 605737; -
DR GO; GO:0005622; C:intracellular; IC.
DR GO; GO:0008189; F:apoptosis inhibitor activity; NAS.
DR GO; GO:0019899; F:enzyme binding; NAS.
DR GO; GO:0007257; P:activation of JUNK; NAS.
DR GO; GO:0006309; P:DNA fragmentation; NAS.
DR GO; GO:0001719; P:inhibition of caspase activation; IEP.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Alternative splicing.
FT REPEAT 90 155 BIR.
FT ZN_FING 252 286 RING-TYPE.
FT DOMAIN 64 69 POLY-GLU.
FT VARSPLIC 1 149 MGPKDSAKLHRGPQPSHWAAGDPTQERCGPRSLGSPVLG
FT LDTCAWDHVDGQILGOLRPLTEEEEGAGATLSRGPAFP
FT GMGSEELRLASFYDWPLTAEVPPPELLAAAGFFHTGHQDKVR
FT CFFCYGGLQSWKRGDDPWTEHAKWFP -> MPLPWDYPEAP
FT WRLHSSPPRCPRALQGGRRGNPDPRGSKGLKQTVGAL
FT NPNLHLWGIC (in isoform 3).
FT /FTid=VSP_002458.
FT Missing (in isoform 1).
FT /FTid=VSP_002459.
FT EE->AA: NO CHANGE IN SMAC INTERACTION AND
FT ANTI-APOPTOTIC ACTIVITY.
FT D->A: ABOLISHES INHIBITION OF CASPASES,
FT SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT C->A: ABOLISHES INHIBITION OF CASPASES
FT AND ANTI-APOPTOTIC ACTIVITY.

Query Match 45.9%; Score 177; DB 1; Length 298;
Best Local Similarity 47.8%; Pred. No. 7.8e-14;
Matches 32; Conservative 9; Mismatches 24; Indels 2; Gaps 1;
QY 2 EARIVTFCGW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPPWDQHAKC 59
Db 88 ELRLASFYDWPLTAEVPPPELLAAAGFFHTGHQDKVRCFFCYGGLQSWKRGDDPWTEHAKW 147

QY 60 YPGCKYL 66
Db 148 FPSCQFL 154

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:48:59 ; Search time 36 Seconds
(without alignments)
578.450 Million cell updates/sec

Title: US-09-654-743-24
Perfect score: 386
Sequence: 1 YEARIVTFTWIYSVNKEQL.....KPSEDPWDQHAQCYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	94.8	496	11 Q9ESF0	Q9esf0 rattus norv
2	366	94.8	501	11 Q9EQ04	Q9eq04 rattus norv
3	361	93.5	501	11 Q9EQ05	Q9eq05 rattus norv
4	306	79.3	106	4 Q96RW6	Q96rw6 homo sapien
5	279	72.3	493	13 Q8UVF8	Q8uvf8 gallus gall
6	258	66.8	109	6 Q8WMY4	Q8wmy4 bos taurus
7	212	54.9	405	13 Q8UWH2	Q8uwH2 brachydanio
8	212	54.9	415	13 Q7SXU1	Q7sxu1 brachydanio
9	192	49.7	195	13 Q9IA70	Q9ia70 gallus gall
10	192	49.7	197	13 Q9IA69	Q9ia69 gallus gall
11	192	49.7	602	11 Q9ESE9	Q9ese9 rattus norv
12	192	49.7	610	13 Q57319	Q57319 gallus gall
13	189	49.0	374	11 Q921N0	Q921n0 mus musculu
14	189	49.0	616	13 Q804E2	Q804e2 ictalurus p
15	189	49.0	628	13 Q8UWD2	Q8uwd2 brachydanio
16	189	49.0	647	13 Q7T0K2	Q7t0k2 brachydanio

17	185	47.9	346	5 Q968T8	Q968t8 bombyx mori
18	185	47.9	346	5 Q8IS31	Q8is31 bombyx mori
19	185	47.9	589	11 Q9QZC6	Q9qzc6 rattus norv
20	185	47.9	589	11 Q9ESE8	Q9ese8 rattus norv
21	183	47.4	534	4 Q8IZZ0	Q8izz0 homo sapien
22	180	46.6	263	12 Q80SP4	Q80sf4 hyphantria
23	180	46.6	283	12 Q80LK8	Q80lk8 adxophyes
24	180	46.6	403	5 Q8WRD9	Q8wrd9 aedes trise
25	178	46.1	438	5 Q9VUX5	Q9vux5 drosophila
26	177	45.9	261	12 Q9QES9	Q9qes9 epiphyas po
27	177	45.9	264	12 Q9EN27	Q9en27 amsacta moo
28	177	45.9	379	5 Q9U492	Q9u492 trichoplusi
29	176	45.6	377	5 Q9NJ07	Q9nj07 spodoptera
30	175	45.3	401	13 Q8JHV9	Q8jHV9 xenopus lae
31	173	44.8	255	12 Q7TSS1	Q7t5s1 cryptophleb
32	173	44.8	324	13 Q9DDN2	Q9ddn2 gallus gall
33	171	44.3	281	12 Q9YNL8	Q9ynl8 choristoneu
34	170	44.0	402	5 Q8T621	Q8t621 aedes albop
35	167	43.3	213	5 Q8MVN1	Q8mvn1 boltenia vi
36	164.5	42.6	276	12 Q89744	Q89744 buzura supp
37	164.5	42.6	1403	11 Q8CH68	Q8ch68 mus musculu
38	164.5	42.6	1403	11 Q8CH64	Q8ch64 mus musculu
39	163.5	42.4	597	11 Q9R015	Q9r015 mus musculu
40	163.5	42.4	1402	11 Q8CH65	Q8ch65 mus musculu
41	163.5	42.4	1402	11 Q8CGT4	Q8cgt4 mus musculu
42	163.5	42.4	1402	11 Q8CGT3	Q8cgt3 mus musculu
43	163.5	42.4	1403	11 Q8CH70	Q8ch70 mus musculu
44	163.5	42.4	1403	11 Q8CGT2	Q8cgt2 mus musculu
45	163.5	42.4	1403	11 Q8BG68	Q8bg68 mus musculu

ALIGNMENTS

RESULT 1
Q9ESF0
ID Q9ESF0 PRELIMINARY; PRT; 496 AA.
AC Q9ESF0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183429; AAC22969.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 94.8%; Score 366; DB 11; Length 496;
Best Local Similarity 93.9%; Pred. No. 5.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 264 YDARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
Q9EQ04 PRELIMINARY; PRT; 501 AA.
AC Q9EQ04;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304334; AAG41193.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query Match 94.8%; Score 366; DB 11; Length 501;
Best Local Similarity 93.9%; Pred. No. 5.9e-35;
Matches 62; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 264 YDARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;

RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAG41192.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28E81C5A0 CRC64;

Query Match 93.5%; Score 361; DB 11; Length 501;
Best Local Similarity 92.4%; Pred. No. 2.3e-34;
Matches 61; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCY 60
Db 264 YDARIIVTFTWISYVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
Q96RW6 PRELIMINARY; PRT; 106 AA.
AC Q96RW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE IAP-like protein 3.
GN ILP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RT "Molecular cloning of human homologs of IAP-like protein."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164681; AAK81891.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
SQ SEQUENCE 106 AA; 12360 MW; 6BBAD3AEA880A891 CRC64;

Query Match 79.3%; Score 306; DB 4; Length 106;
Best Local Similarity 91.1%; Pred. No. 1.4e-28;
Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 WIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKCYPGCKYL 66
Db 2 WIYSVNKEQLSRAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWOHAKWHPGCKYL 57

RESULT 5
Q8UVF8

ID Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
(IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF451854; AAL47170.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CE6119BC CRC64;

Query Match 72.3%; Score 279; DB 13; Length 493;
Best Local Similarity 71.2%; Pred. No. 1.2e-24;
Matches 47; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 YEARIVTFGTWYVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWDQHAKCY 60
Db YERRIQTFLAWIYPVNVKEHLAEAGFYSTGNGDHVVCFHCGGGLQEWKENEDPDWQHAKWF 323

QY 61 PGCKYL 66
Db 324 PGCKFL 329

RESULT 6
Q8WMY4 PRELIMINARY; PRT; 109 AA.
ID Q8WMY4
AC Q8WMY4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN XIAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R.,
RA Jimenez A., Pintado B., De la Fuente J.;
RT "Hyperglycemia-induced apoptosis affects sex ratio of preimplantation
embryos.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458770; AAL66179.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213DE6D CRC64;

Query Match 66.8%; Score 258; DB 6; Length 109;
Best Local Similarity 91.7%; Pred. No. 7.2e-23;
Matches 44; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIVTFGTWYVNVKEQLARAGFYALGEGDKVKCFHCGGLTDWKP 48
Db 57 YEARIITFTWYVNVKEQLARAGFYALGEGDKVKCFHCGGGLNDWKP 104

RESULT 7
Q8UWH2 PRELIMINARY; PRT; 405 AA.
ID Q8UWH2
AC Q8UWH2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Xiap.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF439767; AAL32047.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;

Query Match 54.9%; Score 212; DB 13; Length 405;
Best Local Similarity 51.5%; Pred. No. 8.6e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVTFGTWYVNVKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60
Db 229 FEGRLDSFKGRQHPIDPERLARAGFYSTGEQDVMCFRCGGGVKAWMPDEDPPWEEHARHY 288

QY 61 PGCKYL 66
Db 289 PGCSFL 294

RESULT 8
Q7SXU1 PRELIMINARY; PRT; 415 AA.
ID Q7SXU1

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AC Q7SXUL;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055246; AAH55246.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 415 AA; 46788 MW; D9B82E448ADDDCA92 CRC64;

Query Match 54.9%; Score 212; DB 13; Length 415;
Best Local Similarity 51.5%; Pred. No. 8.9e-17;
Matches 34; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIVTFTGIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAKY 60
Db 240 FEGRIDSFKGRQHPIDPERLARAGFYSTGEQDRVMCFRCGGGVKAWMPDEDPWEHARHY 299

QY 61 PGCKYL 66
Db 300 PGCSPL 305

RESULT 9
Q9IA70 PRELIMINARY; PRT; 195 AA.
AC Q9IA70;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Leghorn; TISSUE=Spleen;
```

```
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes.";
RL Poult. Sci. 80:284-288(2001).
DR EMBL; AF221082; AAF35319.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 49.7%; Score 192; DB 13; Length 195;
Best Local Similarity 52.9%; Pred. No. 9.1e-15;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAK 58
Db 116 HEARVKTFINWPTIPVQPEQLADAGFYVGRNDDVKCFCCDGGRLRCWESGDDPWIEHAK 175

QY 59 CYPGCKYL 66
Db 176 WFPRC EYL 183

RESULT 10
Q9IA69 PRELIMINARY; PRT; 197 AA.
AC Q9IA69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Fayoumi; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes.";
RL Poult. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 49.7%; Score 192; DB 13; Length 197;
Best Local Similarity 52.9%; Pred. No. 9.3e-15;
Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPDQHAK 58
Db 116 HEARVKTFINWPTIPVQPEQLADAGFYVGRNDDVKCFCCDGGRLRCWESGDDPWIEHAK 175
```

Db 117 HEARVKTFINWPTripVQPEQLADAGFYVGRNDDVKFCFCDGGLRCWESGDDPWIEHAK 176

QY 59 CYPGCKYL 66

Db 177 WFPCEYL 184

RESULT 11

Q9ESE9 PRELIMINARY; PRT; 602 AA.

AC Q9ESE9;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Inhibitor of apoptosis protein 1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of

RT Apoptosis Protein 1, 2, and 3 Genes.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AF183430; AAG22970.1; -.

DR HSSP; Q13490; 1QBH.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;

Query Match 49.7%; Score 192; DB 11; Length 602;

Best Local Similarity 51.5%; Pred.No. 3.1e-14;

Matches 35; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIVTFTWIS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58

Db 255 HAARVTFSTWPSALVHPQELASAGFYTGHSDDVKFCFCDGGLRCWESGDDPWIEHAK 314

QY 59 CYPGCKYL 66

Db 315 WFPCEYL 322

RESULT 12

O57319 PRELIMINARY; PRT; 610 AA.

AC O57319;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis

DE PROTEINE).

GN IAP1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

RN NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC STRAIN=WHITE LEHORN; TISSUE=EMBRYONIC FIBROBLAST;

RX MEDLINE=98038801; Pubmed=9372964;

RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;

RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a

RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";

RL Mol. Cell. Biol. 17:7328-7341(1997).

CC -|- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED

CC CELLS.

CC -|- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF

CC THE V-REL-TRANSFORMED CELLS.

CC -|- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE

CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS

CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.

CC -|- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION

CC PROCESS.

CC -|- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.

CC -|- SIMILARITY: MEMBER OF THE IAP FAMILY.

CC -|- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF

CC APOPTOSIS PROTEIN REPEAT).

CC -|- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL; AF008592; AAB88044.1; -.

DR HSSP; Q13490; 1QBH.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.

DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Apoptosis; Zinc-finger; Repeat.

FT REPEAT 30 97 BIR_REPEAT_1.

FT REPEAT 176 242 BIR_REPEAT_2.

FT REPEAT 262 329 BIR_REPEAT_3.

FT ZN FING 563 597 C3HC4-TYPE.

SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 49.7%; Score 192; DB 13; Length 610;

Best Local Similarity 52.9%; Pred.No. 3.2e-14;

Matches 36; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 1 YEARIVTFTW--IYVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPDQHAK 58

Db 262 HEARVKTFINWPTripVQPEQLADAGFYVGRNDDVKFCFCDGGLRCWESGDDPWIEHAK 321

QY 59 CYPGCKYL 66

Db 322 WFPCEYL 329

RESULT 13

Q921N0 PRELIMINARY; PRT; 374 AA.

ID Q921N0;

AC Q921N0;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Similar to baculoviral IAP repeat-containing 2.

GN BIRC2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:09 ; Search time 49.5 Seconds
(without alignments)
376.730 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEARIFTFTGIWYSVNKEQL.....KPSDDPWEQHAQWYPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	66	7	ADB61810 Human inh
2	389	100.0	236	5	ABG32418 X-linked
3	389	100.0	278	5	Aao20511 Protein o
4	389	100.0	497	2	Aaw19581 Human apo
5	389	100.0	497	2	Aaw69294 Human XIA
6	389	100.0	497	3	Aay59451 Human XIA
7	389	100.0	497	3	Aay99985 Human X-1
8	389	100.0	497	5	ABG65663 Human inh
9	389	100.0	497	7	ADB80961 RING-SH c
10	377	96.9	66	7	ADB61827 Rat inhib
11	368	94.6	496	2	Aaw19745 Mouse inh
12	366	94.1	496	2	Aaw19584 Mouse apo
13	366	94.1	496	2	Aaw69297 Murine XI
14	366	94.1	496	5	ABG65666 Mouse inh
15	352	90.5	66	7	ADB61828 Mouse inh
16	352	90.5	496	6	ABP72157 Mouse inh
17	347	89.2	66	7	ADB61820 Human inh
18	347	89.2	236	3	Aay81440 Human TIA
19	347	89.2	236	4	AAE00365 Human IAP
20	347	89.2	236	5	AAU75066 Human tes
21	347	89.2	236	5	ABG32417 Inhibitor
22	347	89.2	464	5	AAU75747 Human Inh
23	341	87.7	236	4	AAE00366 Chimpanze
24	338	86.9	66	7	ADB61831 Gorilla i
25	338	86.9	236	4	AAE00367 Gorilla I

26	322	82.8	57	7	ADB61832 Unidentif
27	287	73.8	66	7	ADB61829 Chicken i
28	255	65.6	52	7	ADB61830 Bovine in
29	216	55.5	68	7	ADB61833 Zebra fis
30	211	54.2	68	7	ADB61813 Human inh
31	211	54.2	557	6	ABP72159 Inhibitor
32	211	54.2	604	2	Aaw19582 Human apo
33	211	54.2	604	2	Aaw19747 Human inh
34	211	54.2	604	2	Aaw13546 Human c-I
35	211	54.2	604	2	Aaw69295 Human HIA
36	211	54.2	604	2	Aay52703 Human cel
37	211	54.2	604	2	Aay33997 Human cel
38	211	54.2	604	5	ABG65664 Human inh
39	211	54.2	604	6	ABU07431 Protein d
40	211	54.2	604	6	ABB82739 Human CIA
41	211	54.2	604	7	ADB80948 RING-SH c
42	211	54.2	604	7	Aae39811 Human cel
43	211	54.2	1140	5	AAU97837 Human cys
44	211	54.2	1141	4	AAAB50694 Human API
45	203	52.2	600	2	AAW69298 Murine HI

ALIGNMENTS

RESULT 1
ADB61810
ID ADB61810 standard; protein; 66 AA.
XX AC ADB61810;
XX DT 04-DEC-2003 (first entry)
XX DE Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; human; BIR 3 domain.
XX KW Wilm's tumour; human; BIR 3 domain.
OS Homo sapiens.
XX WO2003040172-A2.
XX PD 15-MAY-2003.
XX PF 12-NOV-2002; 2002WO-CA001738.
XX PR 09-NOV-2001; 2001US-0332300P.
XX PR 08-APR-2002; 2002US-0370934P.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX PA Boudreault A, Korneluk RG, La Casse E, Liston P;
XX WPI; 2003-513532/48.
XX PT Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX PS Disclosure; Fig 1A; 53pp; English.
XX CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in

embryonic development, viral pathogenesis, cancer, autoimmune disorders and neurodegenerative diseases. The failure of the apoptotic response has been implicated in the development of cancer, autoimmune disorders (for example systemic lupus erythematosus and multiple sclerosis) and viral infections (including herpes virus, poxvirus and adenovirus). The inhibitors of apoptosis (IAPs) are a family of proteins possessing one or more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1 (cIAP2) and HIAP2 (cIAP1) all possess three BIR domains and a carboxy terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and -9 which are proteases involved in the initiation of apoptosis. Compounds which inhibit the activity of IAPs may therefore have cytostatic activity through the enhancement of apoptosis. The polypeptides of the invention are candidate peptide ligands for binding to the BIR domain of IAPs. They may be useful for the treatment of cancer and other neoplasms, such as leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular cancer, small cell lung carcinoma, renal cell carcinoma and Wilm's tumour, and for enhancing apoptosis. The present sequence is that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain against which the peptides of the invention are targeted to bind.

RESULT 2	
ABG32418	
ID	ABG32418 standard; protein; 236 AA.
XX	
AC	ABG32418;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	x-linked inhibitor of apoptosis protein, XIAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor;
KW	fertility; testicular cancer; male infertility; male birth control;
KW	x-linked inhibitor of apoptosis protein; XIAP.
XX	
OS	Mammalia.
XX	
FH	Key
FT	Misc-difference 1
FT	/note= "Encoded by nnn; start codon is illegible in
FT	specification"
XX	
PN	US2002086409-A1.
XX	
PD	04-JUL-2002.
XX	
PF	18-DEC-2001; 2001US-00024433.
XX	
PR	29-JAN-1998; 98US-0073001P.
PR	29-JAN-1999; 99US-00239867.
XX	
PA	(KOEN/) KORNELUK R G.
PA	(LAGA/) LAGACE M.
XX	
PI	Korneluk RG, Lagace M;
XX	
DR	WPI; 2002-642245/69.
DR	N-PSDB; ABS52803.
XX	

Novel polypeptide, a member of inhibitor of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells, particular cells involved in male fertility.

Example 3; Fig 4B; 24pp; English.

A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of apoptosis) family of proteins that is expressed in the testes. (I) is useful for identifying a compound that modulates TIAP biological activity (I) is useful for increasing apoptosis in a cell, preferably a germ-line cell and for increasing fertility in an animal. (I) is useful for treating or preventing apoptosis which occurs as a part of testicular cancer and male infertility. TIAP may be manipulated for use as a male birth control. TIAP polypeptides and nucleic acid sequences also have diagnostic use in the detection or monitoring of conditions involving aberrant levels of apoptosis. The present sequence represents the amino acid sequence of X-linked inhibitor of apoptosis protein, XIAP

Sequence 236 AA;

RESULT 3	
AAO20511	
ID	AAO20511 standard; protein; 278 AA.
XX	
XX	AAO20511;
XX	
XX	27-JUN-2002 (first entry)
XX	
DE	Protein of APP related human homologue hCP35211.
XX	
KW	Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW	amyloid precursor protein; tissue-specific expression control; human APP;
KW	APP pathway modulator; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200226820-A2.
XX	
PD	04-APR-2002.
XX	
PF	01-OCT-2001; 2001WO-EP011345.
XX	
PR	29-SEP-2000; 2000US-0236893P.
PR	14-JUN-2001; 2001US-0298309P.
XX	
PA	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX	
PI	Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI	Reinhardt MWHM, Zusman S;
XX	
DR	WPI; 2002-315796/35.
DR	N-PSDB; AAK99405.
XX	
PT	New transgenic fly, containing DNA encoding an Abeta portion of human
PT	APP, useful for identifying agents which modulate the APP pathway and
PT	which can be used to treat Alzheimer's disease.
XX	
PS	Example 4; Page 112; 129pp; English.
XX	

CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specific expression. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This sequence represents the
CC protein of the APP related human homologue hCP35211
XX
SQ Sequence 278 AA;

Query Match 100.0%; Score 389; DB 5; Length 278;
Best Local Similarity 100.0%; Pred. No. 6.7e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
Db 46 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 105
QY 61 PGCKYL 66
Db 106 PGCKYL 111

RESULT 4
AAW19581
ID AAW19581 standard; protein; 497 AA.

AC AAW19581;
XX
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor XIAP.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain 26..93
FT /label= BIR-1
FT Domain 163..230
FT /label= BIR-2
FT Domain 265..330
FT /label= BIR-3
FT Domain 439..484
FT /label= Ring_zinc_finger

PN WO9706255-A2.
XX
XX
PD 20-FEB-1997.
XX
XX
PF 05-AUG-1996; 96WO-IB001022.
XX
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
PI
XX
DR WPI; 1997-154262/14.
DR N-PSDB; AAT70836.

PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.

XX
PS Claim 27; Page 68-70; 219pp; English.

XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
CC (AAW19581-86) are a new class of mammalian proteins that are inhibitors
CC of apoptosis (IAP) and which are characterised by the presence of a ring
CC zinc finger domain (see also AAW19587) and at least one BIR (baculovirus
CC IAP repeat) domain (see also AAW19588). The XIAP amino acid sequence was
CC deduced from the xiap gene (AAT70836) isolated from a human foetal brain
CC cDNA library. IAP polypeptides can be expressed in host cells (in vitro
CC or in vivo) and used in methods for treating diseases and disorders
CC involving apoptosis, esp. in a human diagnosed as HIV-positive or as
CC having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or
CC an ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease
XX
SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
Db 265 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 5
AAW69294
ID AAW69294 standard; protein; 497 AA.

XX
AC AAW69294;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human XIAP protein.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein.

XX Homo sapiens.
OS
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB0000781.
XX
PR 13-FEB-1997; 97US-00800929.
XX
XX (UYOT-) UNIV OTTAWA.

XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
PI
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55038.

XX Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.

XX Disclosure; Fig 1; 147pp; English.

XX This sequence is the human XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with

CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity;
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX
SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
Db 265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 6
AA59451
ID AAY59451 standard; protein; 497 AA.

XX AAY59451;

XX 24-MAR-2000 (first entry)

XX Human XIAP protein sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta.

XX Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-00130378.

XX 13-MAY-1998; 98JP-00130378.

XX (MATS/) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX N-PSDB; AAZ48862.

XX Screening a substance which inhibits combination of the X-linked

XX inhibitor of apoptosis protein.

XX Claim 3; Page 28-30; 43pp; Japanese.

XX This sequence represents the human XIAP protein. The invention relates to
CC a method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,

CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (Transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug
XX
SQ Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 60
Db 265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 324

QY 61 PGCKYL 66

Db 325 PGCKYL 330

RESULT 7

AA59985

ID AAY99985 standard; protein; 497 AA.

XX AC AAY99985;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis.

XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;

XX antiinflammatory; cytostatic; tumour.

XX Homo sapiens.

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-00392580.

XX 09-SEP-1999; 99US-00392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM, Ackermann EJ;

XX WPI; 2000-498201/44.

XX N-PSDB; AAA64901.

XX Antisense compound useful for research reagents, diagnostics, prophylaxis

XX and for treating disorders associated with X-linked inhibitor of

XX apoptosis, modulates expression of X-linked inhibitor of apoptosis.

XX Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis (the
CC present sequence). Modified phosphorothioate 2'-MOE oligonucleotides are
CC more effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
CC expression in cells and tissues in vitro. The oligonucleotides are also
CC useful for treating animals or humans, prone to a disease associated with
CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
CC prophylactically to prevent infection, inflammation or tumour formation

XX Sequence 497 AA;

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKEY 60

Db 265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 60
61 PGCKYL 66
325 PGCKYL 330

QY 61 PGCKYL 66
325 PGCKYL 330

Db 61 PGCKYL 66
325 PGCKYL 330

RESULT 8
ABG65663
ID ABG65663 standard; protein; 497 AA.
XX AC ABG65663;
XX DT 26-AUG-2002 (first entry)
XX DE Human inhibitor of apoptosis, XIAP.
XX DE Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX OS Homo sapiens.
XX PN WO200226968-A2.
XX PD 04-APR-2002.
XX PF 27-SEP-2001; 2001WO-CA001379.
XX PR 28-SEP-2000; 2000US-00672717.
XX PA (UYOT-) UNIV OTTAWA.
XX PA (AEGE-) AEGERA THERAPEUTICS INC.
XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
XX DR N-PSDB; ABK93869.
XX PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX Example 12; Fig 1; 135pp; English.
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence
XX Sequence 497 AA;
SQ

Query Match 100.0%; Score 389; DB 5; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 60
265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 324

Db 61 PGCKYL 66
325 PGCKYL 330

QY 61 PGCKYL 66
325 PGCKYL 330

Db 61 PGCKYL 66
325 PGCKYL 330

RESULT 9
ADB80961
ID ADB80961 standard; protein; 497 AA.
XX AC ADB80961;
XX DT 04-DEC-2003 (first entry)
XX DE RING-SH complex related protein, SEQ ID No 35.
XX DE RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KW Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsG101;
KW cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KW rhabdovirus; filovirus.
XX OS Unidentified.
XX PN WO2003033646-A2.
XX PD 24-APR-2003.
XX PF 31-JUL-2002; 2002WO-US024589.
XX PR 31-JUL-2001; 2001US-0308958P.
XX PR 09-NOV-2001; 2001US-0345846P.
XX PA (PROT-) PROTEOLOGICS INC.
XX PI Greener T, Moskowitz H, Reiss Y, Alroy I;
XX WPI; 2003-393509/37.
XX DR N-PSDB; ADB81002.
XX PT New isolated protein complex comprising a RING-SH 3 polypeptide and
PT another polypeptide, useful for detecting cells infected with a virus,
PT and for treating viral disorders caused by retroviruses, rhabdoviruses,
PT or filoviruses.
XX Disclosure; Fig 35; 176pp; English.
XX The invention relates to a novel isolated protein complex comprising a
CC RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
CC STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsG101, a cullin, RING-SH, and a
CC clathrin. The novel protein complex has virucide activity and can be used
CC to treat disorders as part of a vaccine. The protein complex and
CC composition are useful for detecting cells infected with a virus, for
CC identifying agents having antiviral activity, and for treating viral
CC disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
CC sequence is a protein comprising the RING-SH complex of the invention.
XX Sequence 497 AA;
SQ

Query Match 100.0%; Score 389; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 60
265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQAKWY 324

Db 61 PGCKYL 66
325 PGCKYL 330

QY 61 PGCKYL 66
325 PGCKYL 330

Db	325	PGCKYL 330	
Db	ADB61827		
RESULT 10			
ID	ADB61827	standard; protein; 66 AA.	
XX	ADB61827;		
AC			
XX			
DT	04-DEC-2003	(first entry)	
XX			
DE	Rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.		
XX			
KW	baculovirus inhibitor of apoptosis repeat domain; BIR domain;		
KW	apoptosis pathway; embryonic development; viral pathogenesis; cancer;		
KW	autoimmune disorder; neurodegenerative disease; apoptotic response;		
KW	systemic lupus erythematosus; multiple sclerosis; viral infection;		
KW	herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;		
KW	HIAP1; CIAP2; HIAP2; CIAP1; RING zinc finger; caspase-3; caspase-7;		
KW	caspase-9; cytostatic; neoplasm; leukemia; colon carcinoma;		
KW	cervical cancer; uterine cancer; testicular cancer;		
KW	small cell lung carcinoma; uterine cancer; renal cell carcinoma;		
KW	Wilm's tumour; BIR 3 domain; rat.		
XX			
OS	Rattus sp.		
XX			
PN	WO2003040172-A2.		
XX			
PD	15-MAY-2003.		
XX			
PF	12-NOV-2002; 2002WO-CA001738.		
XX			
PR	09-NOV-2001; 2001US-0332300P.		
PR	08-APR-2002; 2002US-0370934P.		
XX			
PA	(AEGE-) AEGERA THERAPEUTICS INC.		
XX			
PI	Boudreault A, Korneluk RG, La Casse E, Liston P;		
XX			
DR	WPI; 2003-513532/48.		
XX			
PT	Polypeptide capable of forming a complex with a polypeptide comprising a		
PT	baculovirus inhibitor of apoptosis repeat domain useful for treating		
PT	cancer and other neoplasms.		
XX			
PS	Disclosure; Fig 1B; 53pp; English.		
XX			
CC	This invention relates to a substantially pure polypeptide having a		
CC	length of less than 100 amino acids and capable of forming a complex with		
CC	a polypeptide that includes a baculovirus inhibitor of apoptosis repeat		
CC	(BIR) domain. The apoptosis pathway is known to play a critical role in		
CC	embryonic development, viral pathogenesis, cancer, autoimmune disorders		
CC	and neurodegenerative diseases. The failure of the apoptotic response has		
CC	been implicated in the development of cancer, autoimmune disorders (for		
CC	example systemic lupus erythematosus and multiple sclerosis) and viral		
CC	infections (including herpes virus, poxvirus and adenovirus). The		
CC	inhibitors of apoptosis (IAPs) are a family of proteins possessing one or		
CC	more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1		
CC	(CIAP2) and HIAP2 (CIAP1) all possess three BIR domains and carboxy		
CC	terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and		
CC	-9 which are proteases involved in the initiation of apoptosis. Compounds		
CC	which inhibit the activity of IAPs may therefore have cytostatic activity		
CC	through the enhancement of apoptosis. The polypeptides of the invention		
CC	are candidate peptide ligands for binding to the BIR domain of IAPs. They		
CC	may be useful for the treatment of cancer and other neoplasms, such as		
CC	leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular		
CC	cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma		
CC	and Wilm's tumour, and for enhancing apoptosis. The present sequence is		
CC	that of the rat inhibitor of apoptosis (IAP) protein XIAP BIR3 domain		
CC	which was used to demonstrate homology to human IAP protein BIR domains		
CC	to which the peptides of the invention are targeted to bind.		
XX			
SQ	Sequence 66 AA;		
Query Match	96.9%;	Score 377;	DB 7; Length 66;
Best Local Similarity	95.5%;	Pred. No. 3.7e-38;	
Matches	63; Conservative	2; Mismatches	1; Indels 0; Gaps 0;
QY	1	YEARIFTGTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWEQHAKWY	60
Db	1	YDARIVTFTGTLWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPWEQHAKWY	60
QY	61	PGCKYL 66	
Db	61	PGCKYL 66	
RESULT 11			
AAW19745			
ID	AAW19745	standard; protein; 496 AA.	
XX			
AC	AAW19745;		
XX			
DT	16-SEP-1997	(first entry)	
XX			
DE	Mouse inhibitor of apoptosis protein homologue MIHA.		
XX			
KW	Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;		
KW	degenerative disease; infectious disease; autoimmune disease; cancer;		
KW	therapy; diagnosis.		
XX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	26..93	
FT		/label= BIR	
FT	Region	163..230	
FT		/label= BIR	
FT	Region	264..330	
FT		/label= BIR	
FT	Region	448..485	
FT		/label= RING_finger	
XX			
PN	WO9723501-A1.		
XX			
PD	03-JUL-1997.		
XX			
PF	20-DEC-1996;	96WO-AU000827.	
XX			
PR	22-DEC-1995;	95AU-00007275.	
XX			
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.		
XX			
PI	Vaux DL;		
XX			
DR	WPI; 1997-350966/32.		
DR	N-PSDB; AAT72710.		
XX			
PT	Isolated protein homologues of viral inhibitors of apoptosis - used to		
PT	modulate apoptosis for treatment of degenerative, infectious or		
PT	auto-immune diseases and cancer.		
XX			
PS	Claim 7; Page 44-47; 136pp; English.		
XX			
CC	Mammalian IAP homologue A (MIHA) (AAW19745) is a murine homologue of		
CC	baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence		
CC	was deduced from a cDNA clone (see also AAT72710) isolated from a mouse		
CC	liver cDNA library on the basis of homology to Orgyia pseudotsugata		
CC	polyhedrosis virus IAP BIR and RING finger amino acid motifs (see also		
CC	AAW19744). IAP homologues (see also AAW19746-52) and their derivatives		
CC	and chemical analogues can be used in methods for modulating apoptosis in		
CC	animal cells, specifically for treatment, by inhibition, of degenerative		
CC	and infectious disease or, by promotion, of cancer and autoimmune disease		
XX			
SQ	Sequence 496 AA;		

Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 264 YEARIVTFGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 14
ABG65666
ID ABG65666 standard; protein; 496 AA.
XX
AC ABG65666;
XX
DT 26-AUG-2002 (first entry)
XX
DE Mouse inhibitor of apoptosis, XIAP.
XX
KW Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
KW cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer;
KW embryonic development; viral pathogenesis; autoimmune disorder;
KW neurodegenerative disease; multiple sclerosis; lupus erythematosus;
KW herpes virus infection; pox virus infection; adenovirus infection;
KW proliferative disease.
XX
OS Mus sp.
XX
PN WO200226968-A2:
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
DR N-PSDB; ABK93872.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
PS Example 12; Fig 4; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
XX protein sequence
SQ Sequence 496 AA;

Query Match 94.1%; Score 366; DB 5; Length 496;
Best Local Similarity 95.5%; Pred. No. 8.2e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 264 YEARIVTFGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 15
ADB61828
ID ADB61828 standard; protein; 66 AA.
XX
AC ADB61828;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
XX
KW baculovirus inhibitor of apoptosis repeat domain; BIR domain;
KW apoptosis pathway; embryonic development; viral pathogenesis; cancer;
KW autoimmune disorder; neurodegenerative disease; apoptotic response;
KW systemic lupus erythematosus; multiple sclerosis; viral infection;
KW herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; XIAP;
KW HIAP1; cIAP2; HIAP2; cIAP1; RING zinc finger; caspase-3; caspase-7;
KW caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma;
KW cervical cancer; uterine cancer; testicular cancer;
KW small cell lung carcinoma; uterine cancer; renal cell carcinoma;
KW Wilm's tumour; BIR 3 domain; mouse; murine.
XX
OS Mus sp.
XX
PN WO2003040172-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-CA001738.
XX
PR 09-NOV-2001; 2001US-0332300P.
PR 08-APR-2002; 2002US-0370934P.
XX
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Boudreault A, Korneluk RG, La Casse E, Liston P;
XX WPI; 2003-513532/48.
DR
XX
PS Polypeptide capable of forming a complex with a polypeptide comprising a
PT baculovirus inhibitor of apoptosis repeat domain useful for treating
PT cancer and other neoplasms.
XX
PS Disclosure; Fig 1B; 53pp; English.
XX
CC This invention relates to a substantially pure polypeptide having a
CC length of less than 100 amino acids and capable of forming a complex with
CC a polypeptide that includes a baculovirus inhibitor of apoptosis repeat
CC (BIR) domain. The apoptosis pathway is known to play a critical role in
CC embryonic development, viral pathogenesis, cancer, autoimmune disorders
CC and neurodegenerative diseases. The failure of the apoptotic response has
CC been implicated in the development of cancer, autoimmune disorders (for
CC example systemic lupus erythematosus and multiple sclerosis) and viral
CC infections (including herpes virus, poxvirus and adenovirus. The
CC inhibitors of apoptosis (IAPs) are a family of proteins possessing one or
CC more baculovirus IAP repeat (BIR) domains. Human IAPs, XIAP, HIAP1
CC (cIAP2) and HIAP2 (cIAP1) all posses three BIR domains and carboxy
CC terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and
CC -9 which are proteases involved in the initiation of apoptosis. Compounds
CC which inhibit the activity of IAPs may therefore have cytostatic activity
CC through the enhancement of apoptosis. The polypeptides of the invention

CC are candidate peptide ligands for binding to the BIR domain of IAPs. They
CC may be useful for the treatment of cancer and other neoplasms, such as
CC leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular
CC cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma
CC and Wilm's tumour, and for enhancing apoptosis. The present sequence is
CC that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain
CC which was used to demonstrate homology to human IAP protein BIR domains
CC to which the peptides of the invention are targeted to bind.

xx
SQ Sequence 66 AA;

Query Match 90.5%; Score 352; DB 7; Length 66;
Best Local Similarity 92.4%; Pred. No. 4.1e-35;
Matches 61; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEARIFTGTWYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQWY 60
Db 1 YEARIVTGTWTSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQCY 60

Qy 61 PGCKYL 66
Db 61 PGCKYL 66

Search completed: March 10, 2004, 13:52:28
Job time : 49.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:50:39 ; Search time 16.5 Seconds
(without alignments)
206.504 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEARIFTGTWYISVNKEQL.....KPSDPEWQHAKWYFGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	66	2	US-08-511-485-25 Sequence 25, Appl
2	389	100.0	66	4	US-09-201-936-25 Sequence 25, Appl
3	389	100.0	66	4	US-09-011-356-25 Sequence 25, Appl
4	389	100.0	236	4	US-09-239-867-4 Sequence 4, Appli
5	389	100.0	497	2	US-08-511-485-4 Sequence 4, Appli
6	389	100.0	497	3	US-09-212-971-4 Sequence 4, Appli
7	389	100.0	497	3	US-08-800-929A-4 Sequence 4, Appli
8	389	100.0	497	4	US-09-617-053A-4 Sequence 4, Appli
9	389	100.0	497	4	US-08-657-759-2 Sequence 2, Appli
10	389	100.0	497	4	US-09-201-936-4 Sequence 4, Appli
11	389	100.0	497	4	US-09-011-356-4 Sequence 4, Appli
12	389	100.0	497	4	US-09-672-717-219 Sequence 219, App
13	366	94.1	66	2	US-08-511-485-24 Sequence 24, Appl
14	366	94.1	66	4	US-09-201-936-24 Sequence 24, Appl
15	366	94.1	66	4	US-09-011-356-24 Sequence 24, Appl
16	366	94.1	496	2	US-08-511-485-10 Sequence 10, Appl
17	366	94.1	496	3	US-09-212-971-10 Sequence 10, Appl
18	366	94.1	496	3	US-08-800-929A-10 Sequence 10, Appl
19	366	94.1	496	4	US-09-617-053A-10 Sequence 10, Appl
20	366	94.1	496	4	US-09-201-936-10 Sequence 10, Appl
21	366	94.1	496	4	US-09-011-356-10 Sequence 10, Appl
22	366	94.1	496	4	US-09-672-717-225 Sequence 225, App
23	347	89.2	236	3	US-09-121-979-4 Sequence 4, Appli
24	347	89.2	236	3	US-09-332-319-4 Sequence 4, Appli
25	347	89.2	236	4	US-09-239-867-2 Sequence 2, Appli
26	295	75.8	53	4	US-08-657-759-19 Sequence 19, Appl
27	249	64.0	50	3	US-08-975-080-28 Sequence 28, Appl

28	249	64.0	50	3	US-08-975-080-29 Sequence 29, Appl
29	249	64.0	50	3	US-08-975-080-32 Sequence 32, Appl
30	211	54.2	68	2	US-08-511-485-26 Sequence 26, Appl
31	211	54.2	68	4	US-09-201-936-26 Sequence 26, Appl
32	211	54.2	68	4	US-09-011-356-26 Sequence 26, Appl
33	211	54.2	604	2	US-08-511-485-6 Sequence 6, Appli
34	211	54.2	604	3	US-09-212-971-6 Sequence 6, Appli
35	211	54.2	604	3	US-08-800-929A-6 Sequence 6, Appli
36	211	54.2	604	3	US-08-569-749-4 Sequence 4, Appli
37	211	54.2	604	4	US-09-617-053A-6 Sequence 6, Appli
38	211	54.2	604	4	US-09-201-936-6 Sequence 6, Appli
39	211	54.2	604	4	US-09-011-356-6 Sequence 6, Appli
40	211	54.2	604	4	US-09-672-717-221 Sequence 221, App
41	211	54.2	604	5	PCT-US96-12860-4 Sequence 4, Appli
42	205	52.7	68	2	US-08-511-485-28 Sequence 28, Appl
43	205	52.7	68	4	US-09-201-936-28 Sequence 28, Appl
44	205	52.7	68	4	US-09-011-356-28 Sequence 28, Appl
45	205	52.7	268	3	US-08-836-134-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-25

Query Match 100.0%; Score 389; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHGGGLTDWKPSDPEWQHAKWY 60
|||||

Db 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2

US-09-201-936-25
; Sequence 25, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
Db 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 3

US-09-011-356-25
; Sequence 25, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25

; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-011-356-25

Query Match 100.0%; Score 389; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
Db 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 4

US-09-239-867-4
; Sequence 4, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 100.0%; Score 389; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 8.2e-44;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 60
Db 4 YEARIFTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAHWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69

RESULT 5

US-08-511-485-4
; Sequence 4, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-4

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 PGCKYL 66
Db |||||||
325 PGCKYL 330

RESULT 6
US-09-212-971-4
Sequence 4, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-4

Query Match 100.0%; Score 389; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 265 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAHWY 324
QY 61 PGCKYL 66
Db 325 PGCKYL 330
RESULT 7
US-08-800-929A-4
Sequence 4, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-4

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Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PGCKYL 66
Db 325 PGCKYL 330

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RESULT 8
US-09-617-053A-4
; Sequence 4, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-053A-4

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 60
Db      265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 324

QY      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 9
US-08-657-759-2
; Sequence 2, Application US/08657759
; Patent No. 6511828v
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Duckett, Colin S.
; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS
; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPS)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,759
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 60
Db      265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 324

QY      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 10
US-09-201-936-4
; Sequence 4, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 60
Db      265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAKWY 324

QY      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 11
US-09-011-356-4
; Sequence 4, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-657-759-2

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 10
US-09-201-936-4
; Sequence 4, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match      100.0%; Score 389; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 PGCKYL 66
Db      325 PGCKYL 330

RESULT 11
US-09-011-356-4
; Sequence 4, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
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; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
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; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

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Best Local Similarity 95.5%; Pred. No. 2e-41;
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Db 1 YEARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDWPWEQHAQWY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 15
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; Sequence 24, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 66
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; ORGANISM: Mus musculus
US-09-011-356-24

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Job time : 16.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 389
Sequence: 1 YEARIFTGTWIYSVNKEQL.....KPSQDPWEQHAQWYPGCKYL 66

Scoring table: BLOSUM62
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Searched: 809742 seqs, 211153259 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	389	100.0	66	9 US-09-201-936-25	Sequence 25, Appl
2	389	100.0	107	9 US-09-965-967-20	Sequence 20, Appl
3	389	100.0	278	9 US-09-964-899-39	Sequence 39, Appl
4	389	100.0	497	9 US-09-974-592-4	Sequence 4, Appli
5	389	100.0	497	9 US-09-201-936-4	Sequence 4, Appli
6	366	94.1	66	9 US-09-201-936-24	Sequence 24, Appl
7	366	94.1	496	9 US-09-974-592-10	Sequence 10, Appl
8	366	94.1	496	9 US-09-201-936-10	Sequence 10, Appl
9	249	64.0	50	14 US-10-138-618-28	Sequence 28, Appl
10	249	64.0	50	14 US-10-138-618-29	Sequence 29, Appl
11	249	64.0	50	14 US-10-138-618-32	Sequence 32, Appl
12	211	54.2	68	9 US-09-201-936-26	Sequence 26, Appl
13	211	54.2	604	9 US-09-974-592-6	Sequence 6, Appli
14	211	54.2	604	9 US-09-201-936-6	Sequence 6, Appli
15	211	54.2	604	14 US-10-232-286-4	Sequence 4, Appli

16	54.2	604	14	US-10-141-618-6	Sequence 6, Appli
17	54.2	1140	14	US-10-353-461-8	Sequence 8, Appli
18	52.7	68	9	US-09-201-936-28	Sequence 28, Appl
19	52.7	68	14	US-10-041-859-18	Sequence 18, Appl
20	52.7	172	14	US-10-041-859-12	Sequence 12, Appl
21	52.7	268	14	US-10-323-643-10	Sequence 10, Appl
22	52.2	600	9	US-09-974-592-12	Sequence 12, Appl
23	51.2	68	14	US-10-041-859-14	Sequence 14, Appl
24	51.2	172	14	US-10-041-859-8	Sequence 8, Appli
25	51.2	346	14	US-10-041-859-2	Sequence 2, Appli
26	50.9	68	9	US-09-201-936-27	Sequence 27, Appl
27	50.9	618	9	US-09-974-592-8	Sequence 8, Appli
28	50.9	618	9	US-09-201-936-8	Sequence 8, Appli
29	50.6	438	8	US-08-464-588-2	Sequence 2, Appli
30	50.6	438	14	US-10-323-643-2	Sequence 2, Appli
31	50.6	602	9	US-09-201-936-40	Sequence 40, Appl
32	50.6	612	9	US-09-974-592-14	Sequence 14, Appl
33	50.6	612	14	US-10-232-286-14	Sequence 14, Appl
34	50.6	618	14	US-10-153-668-338	Sequence 338, App
35	50.6	618	14	US-10-207-655-200	Sequence 200, App
36	50.6	618	14	US-10-232-286-2	Sequence 2, Appli
37	49.9	68	14	US-10-041-859-19	Sequence 19, Appl
38	49.9	109	9	US-09-965-967-30	Sequence 30, Appl
39	49.9	172	14	US-10-041-859-13	Sequence 13, Appl
40	49.6	68	14	US-10-041-859-16	Sequence 16, Appl
41	49.6	172	14	US-10-041-859-10	Sequence 10, Appl
42	49.4	68	14	US-10-041-859-15	Sequence 15, Appl
43	49.4	172	14	US-10-041-859-9	Sequence 9, Appli
44	49.1	591	9	US-09-201-936-42	Sequence 42, Appl
45	48.8	68	9	US-09-201-936-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-25
; Sequence 25, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-25

Query Match 100.0%; Score 389; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSQDPWEQHAQWY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 2

US-09-965-967-20
; Sequence 20, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 607236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 607256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-20

Query Match 100.0%; Score 389; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PGCKYL 66
Db 75 PGCKYL 80

RESULT 3

US-09-964-899-39
; Sequence 39, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-964-899-39

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QY 61 PGCKYL 66

Db 106 PGCKYL 111

RESULT 4

US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match 100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 265 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 324

QY 61 PGCKYL 66

Db 325 PGCKYL 330

RESULT 5

US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-201-936-4
Query Match      100.0%; Score 389; DB 9; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 60
Db 265 YEARIFTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 6
US-09-201-936-24
; Sequence 24, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-24

Query Match      94.1%; Score 366; DB 9; Length 66;
Best Local Similarity 95.5%; Pred. No. 9.3e-37;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 60
Db 1 YEARIVTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 60

QY 61 PGCKYL 66
Db 61 PGCKYL 66

RESULT 7
US-09-974-592-10
; Sequence 10, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
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US-09-201-936-10
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10

Query Match      94.1%; Score 366; DB 9; Length 496;
Best Local Similarity 95.5%; Pred. No. 7.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 60
Db 264 YEARIVTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 8
US-09-201-936-10
; Sequence 10, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-10

Query Match      94.1%; Score 366; DB 9; Length 496;
Best Local Similarity 95.5%; Pred. No. 7.9e-36;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 60
Db 264 YEARIVTGTWIVSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAKEY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 9
US-10-138-618-28
; Sequence 28, Application US/10138618
```

Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-138-618-28
Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.3e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWYPGCKYL 40
RESULT 10
US-10-138-618-29
Sequence 29, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-138-618-29
Query Match 64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.3e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWYPGCKYL 66
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWYPGCKYL 40
RESULT 11
US-10-138-618-32
Sequence 32, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,618
FILING DATE: 06-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

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;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-138-618-32

Query Match      64.0%; Score 249; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.3e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 66
   |||||||
Db 1 ALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWYPGCKYL 40

RESULT 12
US-09-201-936-26
; Sequence 26, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-26

Query Match      54.2%; Score 211; DB 9; Length 68;
Best Local Similarity 57.4%; Pred. No. 5e-18;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQ 58
   : || || | || || || || || || || || || || || || || || || || || || ||
Db 1 HAARFKTFFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWWVQHAQ 60

QY 59 WYPGCKYL 66
   | : | : |
Db 61 WFPRCYLY 68

RESULT 13
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
```

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; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6

Query Match      54.2%; Score 211; DB 9; Length 604;
Best Local Similarity 57.4%; Pred. No. 5.1e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQ 58
   : || || | || || || || || || || || || || || || || || || || || || ||
Db 255 HAARFKTFFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWWVQHAQ 314

QY 59 WYPGCKYL 66
   | : | : |
Db 315 WFPRCYLY 322

RESULT 14
US-09-201-936-6
; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-6

Query Match      54.2%; Score 211; DB 9; Length 604;
Best Local Similarity 57.4%; Pred. No. 5.1e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQ 58
   : || || | || || || || || || || || || || || || || || || || || || ||
Db 255 HAARFKTFFNWPSSVLVNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWWVQHAQ 314

QY 59 WYPGCKYL 66
   | : | : |
Db 315 WFPRCYLY 322

RESULT 15
US-10-232-286-4
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Search completed: March 10, 2004, 13:56:59
Job time : 29 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:49:29 ; Search time 13 Seconds
(without alignments)
488.357 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEARIFTGTWIYSVNKEQL.....KPSDDPWEQHAHWPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	389	100.0	497	2	S69544	apoptosis inhibito
2	211	54.2	604	2	S68449	apoptosis inhibito
3	209	53.7	358	2	JC5964	apoptosis inhibito
4	205	52.7	268	2	T10304	inhibitor of apopt
5	205	52.7	268	2	A53989	apoptosis-inhibiti
6	198	50.9	618	2	S68450	apoptosis inhibito
7	190	48.8	275	2	A45679	inhibitor-of-apopt
8	188	48.3	298	2	JC7568	kidney inhibitor o
9	177.5	45.6	1232	2	A55478	neuronal apoptosis
10	174.5	44.9	1447	2	T42628	neuronal apoptosis
11	162	41.6	496	2	S68452	apoptosis inhibito
12	162	41.6	497	2	S69545	apoptosis inhibito
13	144	37.0	208	2	T03183	probable apoptosis
14	139	35.7	150	2	T28409	ORF MSV248 probabl
15	125	32.1	275	2	T10310	apoptosis-inhibiti
16	115.5	29.7	4845	2	T31067	BIR repeat contain
17	111	28.5	286	2	D36828	crf13 protein - Au
18	109	28.0	292	2	T41772	IAP1 orf27 - Bomby
19	101	26.0	155	2	T30489	apoptosis inhibito
20	100	25.7	155	2	T37471	apoptosis inhibito
21	97	24.9	308	2	T37474	apoptosis inhibito
22	87.5	22.5	329	2	T28403	ORF MSV242 probabl
23	87.5	22.5	997	2	T43523	cut17 protein - fi
24	79.5	20.4	564	2	C42523	A55R protein - vac
25	79.5	20.4	564	2	JQ1792	SalF17R protein -
26	66	17.0	576	1	ACFFA2	nicotinic acetylch
27	65	16.7	249	2	H72858	apoptosis inhibito
28	65	16.7	444	2	T15907	hypothetical prote
29	65	16.7	1808	2	T115099	hypothetical prote

30	64.5	16.6	557	2	S12359	nicotinic acetylch
31	64.5	16.6	737	2	PQ0219	RNA-2 polyprotein
32	63.5	16.3	506	2	S13720	coat protein - ara
33	63.5	16.3	607	2	T39823	hypothetical prote
34	63	16.2	234	2	T30427	probable apoptosi
35	62.5	16.1	324	2	S39502	vegetative storage
36	62.5	16.1	532	2	A32751	speract receptor p
37	62	15.9	249	2	T41814	IAP2 orf71 - Bomby
38	62	15.9	474	2	S28419	lamin B-3 - mouse
39	62	15.9	592	2	B48315	lamin B2 - mouse
40	61	15.7	511	2	T43634	nicotinic acetylch
41	61	15.7	534	2	T25720	hypothetical prote
42	61	15.7	776	2	T29064	hyaluronate lyase
43	60	15.4	204	2	H70609	probable dna-3-met
44	60	15.4	246	2	I50127	MHC class II histo
45	60	15.4	252	2	I50126	MHC class II histo

ALIGNMENTS

RESULT 1

S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Duckett, C.S.; Naya, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, E.M.O. J. 15, 2585-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene an
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32974; NID:424-497 <LIS>
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farah.
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161,'C',163-422,'Q',424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:gl184319; PIDN:AAC50373.1; PID:gl184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 389; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 7.8e-37;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAHWY 60

Db 265 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAHWY 324

QY 61 PGCKYL 66

Db 325 PGCKYL 330

RESULT 2

S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farah.

Search completed: March 10, 2004, 13:55:04
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:42:54 ; Search time 10.5 Seconds
(without alignments)
327.298 Million cell updates/sec

Title: US-09-654-743-25

Perfect score: 389

Sequence: 1 YEARIPTFGTWIYSVNKEQL.....KPSDDPWEQHAQWYPGCKYL 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	497	1 BIR4 HUMAN	P98170 homo sapien
2	377	96.9	496	1 BIR4 RAT	Q9r0i6 rattus norv
3	368	94.6	496	1 BIR4 MOUSE	Q60989 mus musculus
4	347	89.2	236	1 BIR8 HUMAN	Q96p09 homo sapien
5	341	87.7	236	1 BIR8 PANTR	Q95m72 pan troglod
6	338	86.9	236	1 BIR8 GORGO	Q95m71 gorilla gor
7	211	54.2	604	1 BIR3 HUMAN	Q13489 homo sapien
8	209	53.7	358	1 PIAP PIG	Q62640 sus scrofa
9	205	52.7	268	1 IAP3 NPVOP	P41437 oryvia pseu
10	204	52.4	611	1 BIR CHICK	Q90660 gallus gall
11	203	52.2	600	1 BIR3 MOUSE	Q08863 mus musculus
12	197	50.6	612	1 BIR2 MOUSE	Q62210 mus musculus
13	197	50.6	618	1 BIR2 HUMAN	Q13490 homo sapien
14	194	49.9	438	1 IAP1 DROME	Q24306 drosophila
15	190	48.8	275	1 IAP GVCP	P41436 cydia pomon
16	188	48.3	298	1 BIR7 HUMAN	Q96ca5 homo sapien
17	178.5	45.9	1403	1 BIRF MOUSE	Q9jib6 mus musculus
18	177.5	45.6	1402	1 BIRG MOUSE	Q9jib3 mus musculus
19	177.5	45.6	1403	1 BIR1 HUMAN	Q13075 homo sapien
20	177.5	45.6	1403	1 BIRA MOUSE	Q9qwk5 mus musculus
21	177.5	45.6	1403	1 BIRE MOUSE	Q9r0i6 mus musculus
22	174.5	44.9	1447	1 BIRB MOUSE	Q9qk4 mus musculus
23	162	41.6	498	1 IAP2 DROME	Q24307 drosophila
24	144	37.0	208	1 ZFP IRV6	P47732 chilo iride
25	129.5	33.3	142	1 BIR5 RAT	Q9jhy7 rattus norv
26	125	32.1	275	1 IAP1 NPVOP	O10296 oryvia pseu
27	121.5	31.2	140	1 BIR5 MOUSE	O70201 mus musculus
28	118.5	30.5	142	1 BIR5 HUMAN	O15392 homo sapien
29	115.5	29.7	4829	1 BIR6 HUMAN	Q9nr09 homo sapien
30	111	28.5	286	1 IAP1 NPVAC	P41435 autographa
31	87.5	22.5	997	1 BIR1 SCHPO	O14064 schizosacch
32	79.5	20.4	564	1 VA55 VACCC	P21073 vaccinia vi
33	79.5	20.4	564	1 VA55 VACCV	P24768 vaccinia vi

ALIGNMENTS

RESULT 1

BIR4_HUMAN	18.4	224	1	IAPL_ASFB7	Q65138 african swi
AC P98170; Q9NQ14;	70.5	224	1	IAPL_ASFM1	O11452 african swi
DT 01-OCT-1996 (Rel. 34, Created)	66.5	224	1	IAPL_ASFCH	O12407 african swi
DT 01-OCT-1996 (Rel. 34, Last sequence update)	66	576	1	ACH2_DROME	P17644 drosophila
DT 10-OCT-2003 (Rel. 42, Last annotation update)	65.5	238	1	IAPL_ASFM2	O11453 african swi
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein) (X-linked IAP)	65	249	1	IAP2_NPVAC	P41454 autographa
DE (IAP-like protein) (HILP).	64.5	557	1	ACH1_SCHGR	P23414 schistocerc
DE BIR4 OR API3 OR IAP3 OR XIAP.	63.5	506	1	POL2_ARMV	P24819 arabis mosa
OS Homo sapiens (Human).	63.5	607	1	PESC_SCHPO	O60164 schizosacch
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	62.5	224	1	IAPL_ASFC3	O11451 african swi
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	62.5	436	1	ACHX_ONCVO	P54247 onchocerca
OX NCBI_TaxID=9606;	62.5	532	1	SPER_STRPU	P16264 strongyloce
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Fetal brain;					
RX MEDLINE=96149249; PubMed=8552191;					
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,					
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;					
RT "Suppression of apoptosis in mammalian cells by NAIP and a related					
RT family of IAP genes.";					
RL Nature 379:349-353(1996).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Fetal heart;					
RX MEDLINE=96256286; PubMed=8654366;					
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,					
RA Gilfillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;					
RT "A conserved family of cellular genes related to the baculovirus iap					
RT gene and encoding apoptosis inhibitors.";					
RL EMBO J. 15:2685-2694(1996).					
RN [3]					
RP SEQUENCE FROM N.A.					
RA Grafham D.;					
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.					
RN [4]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Uterus;					
RX MEDLINE=22388257; PubMed=12477932;					
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,					
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,					
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442;
RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases."
RL Nature 388:300-304(1997).
RN [6]
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "HtrA2 promotes cell death through its serine protease activity and
its ability to antagonize inhibitor of apoptosis proteins."
RL J. Biol. Chem. 277:445-454(2002).
RN [7]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637;
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
RA Herrmann J., Wu J.C., Fesik S.W.;
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
domain."
RL Nature 408:1004-1008(2000).
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
inhibit apoptotic suppressor activity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
LEUKOCYTES.
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
and third BIR domains.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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DR EMBL; U45880; AAC50373.1; -.
DR EMBL; U32974; AAC50518.1; -.
DR EMBL; AL121601; CAB95312.1; -.
DR EMBL; BC032729; AAH32729.1; -.
DR PIR; S69544; S69544.
DR PDB; 1G3F; 10-JAN-01.
DR PDB; 1C9Q; 09-AUG-00.
DR PDB; 1F9X; 11-JUL-01.
DR PDB; 1G73; 10-JAN-01.
DR PDB; 1I30; 26-SEP-01.
DR PDB; 1I40; 31-OCT-01.
DR PDB; 1I51; 23-FEB-02.
DR PDB; 1KMC; 16-JAN-02.
DR Genew; HGNC:592; BIRC4.
DR MIM; 300079; -.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT MUTAGEN 214 214 D->S: REDUCED INTERACTION WITH PRSS25.
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND
WITH PRSS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 Q -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 100.0%; Score 389; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 7.9e-38;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWY 60
Db 265 YEARIFTGTWYVYNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHKWY 324

QY 61 PGCKYL 66
Db 325 PGCKYL 330

RESULT 2
BIR4_RAT
ID BIR4_RAT STANDARD; PRT; 496 AA.
AC Q9R0I6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIRC4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
(By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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DR EMBL; AB033366; BAAS5304.1; -.
DR HSSP; Q13490; IQBH.


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DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 96.9%; Score 377; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2e-36;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIPTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQWY 60
Db 264 YDARIVTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
BIR4_MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60989; O08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIRC4 OR API3 OR XIAP OR AIPA OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSSP; Q13490; IQBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

Query Match 94.6%; Score 368; DB 1; Length 496;
Best Local Similarity 95.5%; Pred. No. 2.2e-35;
Matches 63; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEARIPTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQWY 60
Db 264 YEARIPTGTWISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDPEQHAQWY 323

QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
BIR8_HUMAN
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC Q96P09; Q96RW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21481900; PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
```



```
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffrey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX.
CC -!- SUBUNIT: Binds to caspase-9.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Testis specific in normal tissues.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
DR EMBL; AF420440; AAL30369.1; -.
DR EMBL; AF164682; AAK81892.1; -.
DR Genew; HGNC:14878; BIRC8.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT 7 70 BIR.
FT ZN FING 189 224 RING-TYPE.
FT CONFLICT 196 196 Y -> H (IN REF. 2).
FT SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;
SQ
Query Match 89.2%; Score 347; DB 1; Length 236;
Best Local Similarity 84.8%; Pred. No. 2.9e-33;
Matches 56; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 YEARTFTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAQWY 60
Db 4 YEARTLFTGTWYISVKNKEQLARAGFYALGQEDKVKCFHCGGLANWKPKEDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69
RESULT 5
BIR8_PANTR STANDARD; PRT; 236 AA.
AC Q95M72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffrey S.B.,
```

```
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY030052; AAK49776.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT 7 70 BIR.
FT ZN FING 189 224 RING-TYPE.
FT SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;
SQ
Query Match 87.7%; Score 341; DB 1; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.4e-32;
Matches 55; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 YEARTFTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAQWY 60
Db 4 YEARTLFTGTWYISVKNKEQLARAGFYALGQEDKVKCFHCGGLANWKPKEDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69
RESULT 6
BIR8_GORGO STANDARD; PRT; 236 AA.
AC Q95M71;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffrey S.B.,
RA Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -!- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -!- SUBUNIT: Binds to caspase-9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 1 BIR repeat.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY030052; AAK49776.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
KW REPEAT 7 70 BIR.
FT ZN FING 189 224 RING-TYPE.
FT SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;
SQ
Query Match 87.7%; Score 341; DB 1; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.4e-32;
Matches 55; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 YEARTFTGTWYISVKNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHAQWY 60
Db 4 YEARTLFTGTWYISVKNKEQLARAGFYALGQEDKVKCFHCGGLANWKPKEDPWEQHAQWY 63
QY 61 PGCKYL 66
Db 64 PGCKYL 69
```

CC similarity).

CC -!- SUBUNIT: Binds to caspase-9 (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 1 BIR repeat.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC -----

DR EMBL; AY030053; AAK49777.1; -.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 1.

DR SMART; SM00238; BIR; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.

DR PROSITE; PS0143; BIR_REPEAT_2; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS00089; ZF_RING_2; 1.

KW Apoptosis; Zinc-finger.

FT REPEAT 7 70 BIR.

FT ZN FING 189 224 RING-TYPE.

SQ SEQUENCE 236 AA; 27120 MW; C3A70E39EE442E4C CRC64;

Query Match 86.9%; Score 338; DB 1; Length 236;

Best Local Similarity 81.8%; Pred. No. 3.2e-32;

Matches 54; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEARIFTGTWYISVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY 60

Db 4 YEAWLITFTGWNYSVNKEQLARAGFYAIGQEDKIQCFHCGGGLANWKPKEPDWEQHAKWY 63

QY 61 PGCKYL 66

Db 64 PGCKYL 69

RESULT 7

BIR3_HUMAN STANDARD; PRT; 604 AA.

ID Q13489; Q16628; Q9HC27; Q9UP46;

AC 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis

DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex

DE protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (API2).

GN BIRC3 OR API2 OR IAP1 OR MIHC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96128127; PubMed=8548810;

RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;

RT "The TNFR2-TRAF signaling complex contains two novel proteins related

RT to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96149249; PubMed=8552191;

RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,

RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;

RT "Suppression of apoptosis in mammalian cells by NAIP and a related

RT family of IAP genes.";

RL Nature 379:349-353 (1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=96209843; PubMed=8643514;

RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;

RT "Cloning and expression of apoptosis inhibitory protein homologs that

RT function to inhibit apoptosis and/or bind tumor necrosis factor

RT receptor-associated factors.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=99252096; PubMed=10233894;

RA Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,

RA ten Cate J.W., Pannekoek H.;

RT "Vascular endothelial genes that are responsive to tumor necrosis

RT factor-alpha in vitro are expressed in atherosclerotic lesions,

RT including inhibitor of apoptosis protein-1, stannin, and two novel

RT genes.";

RL Blood 93:3418-3431 (1999).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [6]

RP SEQUENCE OF 362-441 FROM N.A.

RX MEDLINE=20519161; PubMed=11066071;

RA Baens M., Steyls A., Dierlamm J., De Wolf-Peeters C., Marynen P.;

RT "Structure of the MLT gene and molecular characterization of the

RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone

RT B-cell lymphomas of MALT type.";

RL Genes Chromosomes Cancer 29:281-291 (2000).

CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS

CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions

CC inhibit apoptotic suppressor activity.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,

CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.

CC -!- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation

CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid

CC tissue). This translocation is found in approximately 50% of

CC cytogenetically abnormal low-grade MALT lymphoma and involves

CC MALT1 and BIRC3.

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

CC WWW="http://www.infobiogen.fr/services/chroncancer/BIRC3ID239.html".

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EMBL; L49432; AAC41943.1; -
EMBL; U45878; AAC50371.1; -
EMBL; U37546; AAC50507.1; -
EMBL; AF070674; AAC83232.1; -
EMBL; BC037420; AAH37420.1; -
EMBL; AF178945; AAG09369.1; -
PIR; S68449; S68449.
HSSP; Q13490; IQBH.
Genew; HGNC:591; BIRC3.
NIM; 601721; -
GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
REPEAT 29 96 BIR 1.
REPEAT 169 235 BIR 2.
REPEAT 255 322 BIR 3.
DOMAIN 439 529 CARD.
ZNF_RING 557 592 RING-TYPE.
SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM BIRC3-MULTI.
CONFLICT 18 18 N -> Y (IN REF. 4).
CONFLICT 119 119 N -> H (IN REF. 2).
CONFLICT 153 153 D -> E (IN REF. 2).
CONFLICT 163 163 H -> P (IN REF. 2).
CONFLICT 165 165 A -> P (IN REF. 2).
CONFLICT 191 191 K -> R (IN REF. 2).
CONFLICT 364 364 F -> L (IN REF. 2).
CONFLICT 552 552 Q -> P (IN REF. 2).
SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;
Query Match 54.2%; Score 211; DB 1; Length 604;
Best Local Similarity 57.4%; Pred. No. 5.2e-17;
Matches 39; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
Qy 1 YEARIFTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHA 58
Db 255 HAARFKTFNWPSSVLNPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWVQHA 314
Qy 59 WYPGCKYL 66
Db 315 WFPRC EYL 322
RESULT 8
PIAP_PIG STANDARD; PRT; 358 AA.
ID PIAP_PIG
AC O62640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
protein (iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U79142; AAC39171.1; -
CC PIR; JCS964; JCS964.
CC HSSP; Q13490; IQBH.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 2.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 2.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.
CC PROSITE; PS0143; BIR_REPEAT_2; 2.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS50089; ZF_RING_2; 1.
CC Apoptosis; Zinc-finger; Repeat.
CC REPEAT 4 70 BIR 1.
CC REPEAT 90 157 BIR 2.
CC DOMAIN 193 283 CARD.
CC ZNF_RING 311 346 RING-TYPE.
CC SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;
Query Match 53.7%; Score 209; DB 1; Length 358;
Best Local Similarity 55.9%; Pred. No. 5.2e-17;
Matches 38; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
Qy 1 YEARIFTFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHA 58
Db 90 YAARFKTFNWPSSIPVHPEQLASAGFYVGNSSDDVKCFCCDGLRCWESGDDPWVEHA 149
Qy 59 WYPGCKYL 66
Db 150 WFPRC EYL 157
RESULT 9
IAP3_NPVOP STANDARD; PRT; 268 AA.
ID IAP3_NPVOP
AC P41437;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis inhibitor 3 (IAP-3).

FT CONFLICT 183 183 S -> F (IN REF. 2).

FT CONFLICT 190 192 CLW -> FLS (IN REF. 2).

FT CONFLICT 196 196 V -> L (IN REF. 2).

FT CONFLICT 202 203 DD -> YY (IN REF. 2).

FT CONFLICT 213 214 VN -> FT (IN REF. 2).

FT CONFLICT 217 218 VK -> GQ (IN REF. 2).

FT CONFLICT 350 355 WNSSCT -> EQLLS (IN REF. 2).

FT CONFLICT 359 359 K -> T (IN REF. 2).

FT CONFLICT 426 426 E -> D (IN REF. 2).

FT CONFLICT 492 492 T -> K (IN REF. 2).

FT CONFLICT 497 497 S -> L (IN REF. 2).

FT CONFLICT 524 524 F -> C (IN REF. 2).

SQ SEQUENCE 611 AA; 59009 MW; 53FC9136F34EBDD CRC64;

Query Match 52.4%; Score 204; DB 1; Length 611;

Best Local Similarity 54.4%; Pred. No. 3.4e-16;

Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIPTFTGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEOHAK 58

Db 262 HEARKVTFINWPTRIPOPEQLADAGFYVYGRNDDVKCFCCDGLRCWESGDDPWIEHAK 321

QY 59 WYPGCKYL 66

Db 322 WFPCEYL 329

RESULT 11

BIR3_MOUSE

ID BIR3_MOUSE STANDARD; PRT; 600 AA.

AC O08863;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 1) (MIAP1) (MIAP-1).

GN BIRC3 OR BIRC2 OR IAP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE=98110590; PubMed=9441758;

RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;

RT "Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes.";

RL Genomics 46:495-503(1997).

CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).

CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -----

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CC -----

CC EMBL; U88908; AAC53531.1; -.

CC HSSP; Q13490; 1QBH.

CC MGI; MGI:1197007; Birc2.

CC InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR_REPEAT_1; 3.

DR PROSITE; PS0143; BIR_REPEAT_2; 3.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Apoptosis; Zinc-finger; Repeat.

FT REPEAT 27 94 BIR 1.

FT REPEAT 167 233 BIR 2.

FT REPEAT 253 320 BIR 3.

FT DOMAIN 436 525 CARD.

FT ZN_FING 553 588 RING-TYPE.

SQ SEQUENCE 600 AA; 67198 MW; AD7F73EG849317D1 CRC64;

Query Match 52.2%; Score 203; DB 1; Length 600;

Best Local Similarity 52.9%; Pred. No. 4.4e-16;

Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIPTFTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEOHAK 58

Db 253 HAARITFTSNWPSSALVHSQELASAGFYTGHSDVDVKCFCCDGLRCWESGDDPWVEHAK 312

QY 59 WYPGCKYL 66

Db 313 WFPCEYL 320

RESULT 12

BIR2_MOUSE

ID BIR2_MOUSE STANDARD; PRT; 612 AA.

AC Q62210; O08864;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis protein 2) (MIAP2) (MIAP-2).

GN BIRC2 OR BIRC3 OR IAP2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE=96128127; PubMed=8548810;

RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;

RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE=98110590; PubMed=9441758;

RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;

RT "Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes.";

RL Genomics 46:495-503(1997).

CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung, liver, skeletal muscle, kidney and testis.

CC -!- SIMILARITY: Belongs to the IAP family.

CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
CC EMBL; L49433; AAC42078.1; -.
CC EMBL; U88909; AAC53532.1; -.
CC HSSP; Q13490; IQBH.
CC MGD; MGI:1197009; Birc3.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS0209; CARD; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> X (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 612;
Best Local Similarity 52.9%; Pred. No. 2.3e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFTWIYS--VNKEQLARACFYALGEGDKVKCFHCGGGLTDWKPSEDWPQEHAK 58
Db 262 HSARLRTFLYWPSPVQPEQLASAGFYVDRNDVVKCFCCDGLRCWEPGDDPWIEHAK 321

QY 59 WYPGCKYL 66
Db 322 WFPRCFL 329

RESULT 13
BIR2_HUMAN STANDARD; PRT; 618 AA.
AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC2 OR API1 OR IAP2 OR MIHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";

RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE=99332054; PubMed=10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat."
RL Nat. Struct. Biol. 6:648-651(1999).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC EMBL; L49431; AAC41942.1; -.
DR EMBL; U45879; AAC50372.1; -.
DR EMBL; U37547; AAC50508.1; -.
DR EMBL; BC016174; AAH16174.1; -.
DR EMBL; BC028578; AAH28578.1; -.
DR PIR; S68450; S68450.
DR PDB; 1QBH; 20-OCT-99.
DR Genew; HGNC:590; BIRC2.
DR MIM; 601712; -.
DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01433; BIR_REPEAT_2; 3.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
KW REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 543 CARD.
FT ZN FING 571 606 RING-TYPE.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
FT TURN 269 270
FT HELIX 271 274
FT HELIX 287 293
FT TURN 294 294
FT TURN 296 297
FT TURN 301 304
FT STRAND 309 309
FT HELIX 322 325
FT TURN 326 328
FT STRAND 333 333
FT TURN 334 344
FT HELIX 344 351
FT TURN 353 354
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 50.6%; Score 197; DB 1; Length 618;
Best Local Similarity 52.9%; Pred. No. 2.3e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Qy 1 YEARTFTGTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPWEQHA 58
Db 269 HAARMRTFTWYPSVPVQPEQLASAGFYVGRNDVVKCFCCDGLRCWESGDDPWEHAK 328

Qy 59 WYPGCKYL 66
Db 329 WFPRCFL 336

RESULT 14
IAP1_DROME STANDARD; PRT; 438 AA.
AC Q24306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (diap1) (Thread protein).
```

```
GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye imaginal disk;
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A.; Wassarman D.A.; Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RT function to block cell death.";
RL Cell 83:1253-1262(1995).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC -!- HID-DEPENDENT CELL DEATH IN THE EYE.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC -----
CC EMBL; L49440; AAC41609.1; -.
DR PDB; 1JD4; 05-DEC-01.
DR PDB; 1JD5; 05-DEC-01.
DR PDB; 1JD6; 05-DEC-01.
DR FlyBase; FBgn0003691; th.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS01433; BIR_REPEAT_2; 2.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 44 110 BIR 1.
FT REPEAT 226 293 BIR 2.
FT ZN FING 391 426 RING-TYPE.
SQ SEQUENCE 438 AA; 48098 MW; A6C2C8EDF5AEF29 CRC64;

Query Match 49.9%; Score 194; DB 1; Length 438;
Best Local Similarity 48.5%; Pred. No. 3.6e-15;
Matches 32; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

Qy 3 ARIFTFTWYSVNKE--QLARAGFYALGEGDKVKCFHCGGLTDWKPSDEPWEQHA 60
Db 228 ARLRTFEAWPRNLKQKPHQLAEAGFFYTGVDVRVRCFSCGGLMDNDNDPWEQHALWL 287

Qy 61 PGCKYL 66
Db 288 SQCRFV 293

RESULT 15
IAP_GVCP STANDARD; PRT; 275 AA.
AC P41436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis inhibitor IAP.
GN IAP.
```


Search completed: March 10, 2004, 13:53:00
Job time : 10.5 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 13:48:59 ; Search time 36 seconds
(without alignments)
578.450 Million cell updates/sec

Title: US-09-654-743-25
Perfect score: 389
Sequence: 1 YEAFITFTGTWYVNVKEQL.....KPSDDPWEQHAQWPGCKYL 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	377	96.9	496	11 Q9ESF0	Q9esf0 rattus norv
2	377	96.9	501	11 Q9EQ04	Q9eq04 rattus norv
3	372	95.6	501	11 Q9EQ05	Q9eq05 rattus norv
4	322	82.8	106	4 Q96RW6	Q96rw6 homo sapien
5	287	73.8	493	13 Q8UVF8	Q8uvf8 gallus gall
6	255	65.6	109	6 Q8WMY4	Q8wmy4 bos taurus
7	216	55.5	405	13 Q8UWH2	Q8uwh2 brachydanio
8	216	55.5	415	13 Q7SXU1	Q7sxu1 brachydanio
9	206	53.0	602	11 Q9ESE9	Q9ese9 rattus norv
10	204	52.4	195	13 Q9IA70	Q9ia70 gallus gall
11	204	52.4	197	13 Q9IA69	Q9ia69 gallus gall
12	204	52.4	610	13 Q57319	Q57319 gallus gall
13	203	52.2	374	11 Q921N0	Q921n0 mus musculu
14	202	51.9	616	13 Q804E2	Q804e2 ictalurus p
15	202	51.9	628	13 Q8UWD2	Q8uwd2 brachydanio
16	202	51.9	647	13 Q7T0K2	Q7t0k2 brachydanio

17	199	51.2	346	5 Q968T8	Q968t8 bombyx mori
18	199	51.2	346	5 Q8IS31	Q8is31 bombyx mori
19	198	50.9	589	11 Q9QZC6	Q9qzc6 rattus norv
20	198	50.9	589	11 Q9ESE8	Q9ese8 rattus norv
21	197	50.6	534	4 Q8IZZ0	Q8izz0 homo sapien
22	196	50.4	283	12 Q80LK8	Q80lk8 adoxophyes
23	195	50.1	263	12 Q80SF4	Q80sf4 hyphantria
24	195	50.1	403	5 Q8WRD9	Q8wrd9 aedes trise
25	194	49.9	438	5 Q9VUX5	Q9vux5 drosophila
26	193	49.6	379	5 Q9U492	Q9u492 trichoplusi
27	192	49.4	261	12 Q9QES9	Q9ges9 epiphyas po
28	192	49.4	377	5 Q9NJ07	Q9nj07 spodoptera
29	189	48.6	255	12 Q7T5S1	Q7t5s1 cryptophleb
30	189	48.6	264	12 Q9EN27	Q9en27 ansacta moo
31	188	48.3	401	13 Q8JHV9	Q8jhv9 xenopus lae
32	186	47.8	281	12 Q9YNL8	Q9ynl8 choristoneu
33	186	47.8	402	5 Q8T621	Q8t621 aedes albop
34	185	47.6	324	13 Q9DDN2	Q9ddn2 gallus gall
35	180.5	46.4	276	12 Q89744	Q89744 buzura supp
36	180	46.3	213	5 Q8MVN1	Q8mvl boltenia vi
37	178.5	45.9	1403	11 Q8CH68	Q8ch68 mus musculu
38	178.5	45.9	1403	11 Q8CH64	Q8ch64 mus musculu
39	177.5	45.6	597	11 Q9R015	Q9r015 mus musculu
40	177.5	45.6	1402	11 Q8CH65	Q8ch65 mus musculu
41	177.5	45.6	1402	11 Q8CGT4	Q8cgt4 mus musculu
42	177.5	45.6	1402	11 Q8CGT3	Q8cgt3 mus musculu
43	177.5	45.6	1403	11 Q8CH70	Q8ch70 mus musculu
44	177.5	45.6	1403	11 Q8CGT2	Q8cgt2 mus musculu
45	177.5	45.6	1403	11 Q8BG68	Q8bg68 mus musculu

ALIGNMENTS

RESULT 1
Q9ESF0
ID Q9ESF0 PRELIMINARY; PRT; 496 AA.
AC Q9ESF0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183429; AAG22969.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; F:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 96.9%; Score 377; DB 11; Length 496;
Best Local Similarity 95.5%; Pred. No. 2.3e-34;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 264 YDARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 2
Q9EQ04 PRELIMINARY; PRT; 501 AA.
AC Q9EQ04;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304334; AAG41193.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query Match 96.9%; Score 377; DB 11; Length 501;
Best Local Similarity 95.5%; Pred. No. 2.3e-34;
Matches 63; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 264 YDARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 3
Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ovary;
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RA Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAG41192.1; -.
DR HSSP; P98170; 1G3F.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28B81C5A0 CRC64;

Query Match 95.6%; Score 372; DB 11; Length 501;
Best Local Similarity 93.9%; Pred. No. 8.6e-34;
Matches 62; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 60
Db 264 YDARIVTFTGWTIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 323
QY 61 PGCKYL 66
Db 324 PGCKYL 329

RESULT 4
Q96RW6 PRELIMINARY; PRT; 106 AA.
AC Q96RW6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE IAP-like protein 3.
GN ILP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mir S.S., Duckett C.S.;
RT "Molecular cloning of human homologs of IAP-like protein.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164681; AAK81891.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
SQ SEQUENCE 106 AA; 12360 MW; 6BBAD3AEA880A891 CRC64;

Query Match 82.8%; Score 322; DB 4; Length 106;
Best Local Similarity 94.6%; Pred. No. 7.4e-29;
Matches 53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 WIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 66
Db 2 WIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHAQWY 57

RESULT 5
Q9UVF8
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ID Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP (IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF451854; AAL47170.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 73.8%; Score 287; DB 13; Length 493;
Best Local Similarity 71.2%; Pred.No. 3.6e-24;
Matches 47; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHKWY 60
Db 264 YERRIQTFLAWIYPVNKEHLAEAGFYSTGNGDHVVCFHCGGLQEWKENEDPWDQHKWF 323

QY 61 PGCKYL 66
Db 324 PGCKFL 329

RESULT 6
Q8WMY4
ID Q8WMY4 PRELIMINARY; PRT; 109 AA.
AC Q8WMY4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE X-linked inhibitor of apoptosis protein (Fragment).
GN XIAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gutierrez-Adan A., Madrid-Bury N., Arroyo-Garcia R., Fernandez R., Jimenez A., Pintado B., De la Fuente J.;
RT "Hyperglycemia-induced apoptosis affects sex ratio of preimplantation embryos.";
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF458770; AAL66179.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.

DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12361 MW; C4027DC88213DE6D CRC64;

Query Match 65.6%; Score 255; DB 6; Length 109;
Best Local Similarity 91.7%; Pred.No. 2.9e-21;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKP 48
Db 57 YEARIITFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLNDWKP 104

RESULT 7
Q8UWH2
ID Q8UWH2 PRELIMINARY; PRT; 405 AA.
AC Q8UWH2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Xiap.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF439767; AAL32047.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;

Query Match 55.5%; Score 216; DB 13; Length 405;
Best Local Similarity 53.0%; Pred.No. 3.1e-16;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDPWEQHKWY 60
Db 229 FEGRLDSEFKGRQHPIDPERLARAGFYSGEQDRVMCFRCGGGVKAWMPDEDPWEHARHY 288

QY 61 PGCKYL 66
Db 289 PGCSFL 294

RESULT 8
Q7SXU1
ID Q7SXU1 PRELIMINARY; PRT; 415 AA.

AC Q7SXU1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055246; AAH55246.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 415 AA; 46788 MW; D9B82E448ADDCA92 CRC64;

Query Match 55.5%; Score 216; DB 13; Length 415;
Best Local Similarity 53.0%; Pred. No. 3.2e-16;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 YEARIFTGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHWY 60
Db 240 FEGRLDSFKGRQHPIDPERLARAGFYSTGEQDQVRCRCGGGVKAWMPDEDPWEHARHY 299

QY 61 PGCKYL 66
Db 300 PGCSFL 305

RESULT 9
Q9ESE9 PRELIMINARY; PRT; 602 AA.
AC Q9ESE9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of

RT Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183430; AAG22970.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;

Query Match 53.0%; Score 206; DB 11; Length 602;
Best Local Similarity 52.9%; Pred. No. 6.5e-15;
Matches 36; Conservative 10; Mismatches 20; Indels 2; Gaps 1;

QY 1 YEARIFTGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWEQHWY 58
Db 255 HAARVRFSTWPSALVHPQELASAGFYTGHSDDDVKCFCCDGGGLRCWESGDDPWVEHAK 314

QY 59 WYPGCKYL 66
Db 315 WFPRC EYL 322

RESULT 10
Q9IA70 PRELIMINARY; PRT; 195 AA.
AC Q9IA70;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Leghorn; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes.";
RL Poult. Sci. 80:284-288 (2001).
DR EMBL; AF221082; AAF35319.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 52.4%; Score 204; DB 13; Length 195;

Best Local Similarity 54.4%; Pred. No. 3.3e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAH 58
Db :|||:|
116 HEARVKTFINWPTIPVQPEQLADAGFYVGRNDDVKCFCCDGLRCWESGDDPWIEHAK 175
QY 59 WYPGCKYL 66
Db :|||:|
176 WPRCEYL 183

RESULT 11

Q91A69 PRELIMINARY; PRT; 197 AA.
AC Q91A69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bred Fayoumi; TISSUE=Spleen;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes";
RL Poultry. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623BE1A CRC64;

Query Match 52.4%; Score 204; DB 13; Length 197;
Best Local Similarity 54.4%; Pred. No. 3.3e-15;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAH 58
Db :|||:|
117 HEARVKTFINWPTIPVQPEQLADAGFYVGRNDDVKCFCCDGLRCWESGDDPWIEHAK 176
QY 59 WYPGCKYL 66
Db :|||:|
177 WPRCEYL 184

RESULT 12

O57319 PRELIMINARY; PRT; 610 AA.
AC O57319;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis PROTEIN 1 (IAP) (Inhibitor of T cell apoptosis
PROTEINE).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
mediator of the antiapoptotic activity of the v-Rel oncoprotein";
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CELLS.
CC -!- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
THE V-REL-TRANSFORMED CELLS.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -!- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
PROCESS.
CC -!- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -!- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -!- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
APOPTOSIS PROTEIN REPEAT).
CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF008592; AAB88044.1; -.
DR HSSP; Q13490; 1QBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 52.4%; Score 204; DB 13; Length 610;
Best Local Similarity 54.4%; Pred. No. 1.1e-14;
Matches 37; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFGTW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGLTDWKPSDDPWEQHAH 58
Db :|||:|
262 HEARVKTFINWPTIPVQPEQLADAGFYVGRNDDVKCFCCDGLRCWESGDDPWIEHAK 321
QY 59 WYPGCKYL 66
Db :|||:|
322 WPRCEYL 329

RESULT 13

Q921N0 PRELIMINARY; PRT; 374 AA.
AC Q921N0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC011338; AAH11338.1; -.
DR MGD; MGI:1197007; Birc2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; P:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 52.2%; Score 203; DB 11; Length 374;
Best Local Similarity 52.9%; Pred. No. 8.6e-15;
Matches 36; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 YEARIFTFTWYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWQHAK 58
Db 253 HAARITFTFNWPSALVHQSQELASAGFYTGHSDVDVKCFCCDGGGLRCWESGDDPWVEHAK 312
QY 59 WYPGCKYL 66
Db 313 WPRCEYL 320

RESULT 14
Q804E2 PRELIMINARY; PRT; 616 AA.
AC Q804E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN CIAP-1.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Praveen K., Leary J.H. III, Evans D.L., Jaso-Friedmann L.;
RT "Cloning of anti-apoptotic genes in non-specific cytotoxic cells."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY184377; AAO24632.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 616 AA; 69546 MW; D1389D915C6BB256 CRC64;

Query Match 51.9%; Score 202; DB 13; Length 616;
Best Local Similarity 52.2%; Pred. No. 1.9e-14;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIFTFTGW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWQHAKW 59
Db 270 EERLLTFTFNWPARIPVRPDQLAKAGFYVYVGRNDDVKCFCCDGGGLRCWESGDDPWVEHAKW 329
QY 60 YPGCKYL 66
Db 330 FPRCEYL 336

RESULT 15
Q8UWD2 PRELIMINARY; PRT; 628 AA.
AC Q8UWD2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Iap1.
GN IAP1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF442500; AAL33679.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 51.9%; Score 202; DB 13; Length 628;
Best Local Similarity 52.2%; Pred. No. 1.9e-14;
Matches 35; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 2 EARIFTFTGW--IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSDDPWQHAKW 59
Db 280 EERLLTFTFNWPSRIPVRPDQLAKAGFYVYVGRNDDVKCFCCDGGGLRCWESGDDPWVEHAKW 339
QY 60 YPGCKYL 66
Db 340 FPRCEYL 346

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GenCore version 5.1.6
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Listing first 45 summaries

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- 37: em_htg_vrt:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	198	100.0	1588	6	AR263641	AR263641 Sequence
2	198	100.0	1659	6	E31042	E31042 Method for
3	198	100.0	1659	6	AR270490	AR270490 Sequence
4	198	100.0	1659	9	HSU32974	U32974 Human IAP-1
5	198	100.0	2086	6	BC032729	BC032729 Homo sapi
6	198	100.0	2404	6	AX429575	AX429575 Sequence
7	198	100.0	2540	6	AR103281	AR103281 Sequence
8	198	100.0	2540	6	AR302736	AR302736 Sequence
9	198	100.0	2540	6	AR380355	AR380355 Sequence
10	198	100.0	2540	6	AR435471	AR435471 Sequence
11	198	100.0	2540	6	AX412118	AX412118 Sequence
12	198	100.0	2540	6	AX587804	AX587804 Sequence
13	198	100.0	2540	9	HSU45880	U45880 Human X-lin
14	198	100.0	3000	6	AX412131	AX412131 Sequence
15	198	100.0	5232	6	AR106397	AR106397 Sequence
16	198	100.0	5232	6	AR116699	AR116699 Sequence
17	198	100.0	5232	6	AR370617	AR370617 Sequence
18	198	100.0	5232	6	AX670900	AX670900 Sequence
19	198	100.0	5232	6	BD190868	BD190868 Detection
20	180.4	91.1	1752	6	AX104956	AX104956 Sequence
21	180.4	91.1	1752	9	AF164681	AF164681 Homo sapi
22	180.4	91.1	154214	9	AC079753	AC079753 Homo sapi
23	179.4	90.6	1491	10	AF183429	AF183429 Rattus no
24	179.4	90.6	2468	10	AB033366	AB033366 Rattus no
25	179.4	90.6	3032	10	AF304334	AF304334 Rattus no
26	177.8	89.8	2032	10	AF304333	AF304333 Rattus no
27	174.6	88.2	1988	10	MMU36842	U36842 Mus musculu
28	173	87.4	2100	6	AR302739	AR302739 Sequence
29	173	87.4	2100	6	AR435474	AR435474 Sequence
30	173	87.4	2100	6	AX412124	AX412124 Sequence
31	169.8	85.8	2691	6	AR106400	AR106400 Sequence
32	169.8	85.8	2691	6	AR116702	AR116702 Sequence
33	169.8	85.8	2691	6	AR370620	AR370620 Sequence
34	169.8	85.8	2691	6	AX670906	AX670906 Sequence
35	169.8	85.8	2691	6	BD190871	BD190871 Detection
36	169.8	85.8	2691	10	MMU88990	U88990 Mus musculu
37	169.8	85.8	205991	2	AC109227	AC109227 Mus muscu
38	169.8	85.8	208236	2	AC137152	AC137152 Mus muscu
39	166	83.8	711	6	AX104970	AX104970 Sequence
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41	166	83.8	1758	6	AX370787	AX370787 Sequence
42	166	83.8	1758	6	AX370789	AX370789 Sequence
43	166	83.8	4993	6	AX104968	AX104968 Sequence
44	166	83.8	4993	9	AF164682	AF164682 Homo sapi
45	166	83.8	144301	9	AC010467	AC010467 Homo sapi

ALIGNMENTS

RESULT 1
AR263641
LOCUS AR263641 1588 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6331412.
ACCESSION AR263641
VERSION AR263641.1 GI:28075567
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1588)
AUTHORS Korneluk,R.G. and Lagace,M.
TITLE Methods and compounds for modulating male fertility
JOURNAL Patent: US 6331412-A 3 18-DEC-2001;
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 2
E31042 LOCUS E31042 1659 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for screening substance inhibiting binding to XIAP.
ACCESSION E31042
VERSION E31042.1 GI:13017307
KEYWORDS JP 1999326328-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1659)
AUTHORS Kunihiro, M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 199326328-A 2 26-NOV-1999;
COMMENT KUNIHIRO MATSUMOTO
OS Unidentified
PN JP 1999326328-A/2
PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNIHIRO MATSUMOTO
PI G01N33/536, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
PC A61K39/395,
PC A61K45/00, A61K45/00, C07K7/06, C07K7/08, C07K14/47, -PC
G01N33/536,
PC G01N33/536, G01N33/536//C12N15/09, C12P21/08, A61K37/02, A61K37/02, PC
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 82..1572.
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 994 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1053

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3
AR270490 LOCUS AR270490 1659 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1053 from patent US 6500938.
ACCESSION AR270490
VERSION AR270490.1 GI:29701724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1053 31-DEC-2002;
FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180
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QY 181 CCAGGGTGCAAAATATCTG 198
Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 4
HSU32974 LOCUS HSU32974 1659 bp mRNA linear PRI 12-JUN-1996
DEFINITION Human IAP-like protein ILP mRNA, complete cds.
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1659)
AUTHORS Duckett, C.S., Nava, V.E., Gedrich, R.W., Clem, R.J., Van Dongen, J.L., Gilfillan, M.C., Shiels, H., Hardwick, J.M. and Thompson, C.B.
TITLE A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors
JOURNAL EMBO J 15 (11), 2685-2694 (1996)
MEDLINE 96256286
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Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 931 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 990
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 991 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 1050
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1051 CCAGGGTGCAAAATATCTG 1068

RESULT 6
AX429575
LOCUS AX429575 2404 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 38 from Patent WO226820.
ACCESSION AX429575
VERSION AX429575.1 GI:21540833
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusman,S.
TITLE Transgenic drosophila melanogaster expressing beta anyloid
JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
NOVARTIS ERFIND VERWALT GMBH (AT)
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Best Local Similarity 100.0%; Pred. No. 2.6e-44;
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DB 827 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 886
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
DB 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 946
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 947 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 1006
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1007 CCAGGGTGCAAAATATCTG 1024

RESULT 7

AR103281
LOCUS AR103281 2540 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6087173.
ACCESSION AR103281
VERSION AR103281.1 GI:12814869
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
FEATURES
source
1..2540
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAGCCAGTGAGCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 8

AR302736
LOCUS AR302736 2540 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6541457.
ACCESSION AR302736
VERSION AR302736.1 GI:31691179
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.

TITLE Mammalian IAP gene family, primers, probes and detection methods
JOURNAL Patent: US 6541457-A 3 01-APR-2003;
FEATURES Location/Qualifiers
source 1. .2540
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 9
AR380355 AR380355 2540 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 900 from patent US 6507879.
ACCESSION AR380355
VERSION AR380355.1 GI:40087989
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6507879-A 900 19-AUG-2003;
FEATURES Location/Qualifiers
source 1. .2540
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 10
AR435471 AR435471 2540 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 3 from patent US 6566704.
ACCESSION AR435471
VERSION AR435471.1 GI:40198322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
JOURNAL Patent: US 6566704-A 3 02-DEC-2003;
FEATURES Location/Qualifiers
source 1. .2540
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 11
AX412118 AX412118 2540 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,B., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 218 04-APR-2002;
University of Ottawa (CA) ; Aegea Therapeutics Inc. (CA)
FEATURES Location/Qualifiers
source 1. .2540
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.6e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

Db 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 945

QY 121 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 180

Db 946 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198

Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 12

AX587804

LOCUS AX587804 2540 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 274 from Patent WO0246467.

ACCESSION AX587804

VERSION AX587804.1 GI:28212417

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P. and Fert, V.

TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes

JOURNAL Patent: WO 0246467-A 274 13-JUN-2002;

Ipsogen (FR)

FEATURES

source

1. .2540

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="primer"

misc_feature 1. .2540

/note="baculoviral iap repeat-containing 4 (BIRC4) gene."

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2540;

Best Local Similarity 100.0%; Pred. No. 2.6e-44;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 60

Db 826 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 945

QY 121 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 180

Db 946 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198

Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 13

HSU45880

LOCUS HSU45880 2540 bp mRNA linear PRI 16-FEB-1996

DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete cds.

ACCESSION U45880

VERSION U45880.1 GI:1184319

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,

Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., MacKenzie, A. and Korneluk, R.G.

Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes

Nature 379 (6563), 349-353 (1996)

JOURNAL

MEDLINE 96149249

PUBMED 8552191

REFERENCE 2 (bases 1 to 2540)

AUTHORS Baird, S.D.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1, Canada

FEATURES

source

Location/Qualifiers

1. .2540

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/map="Xq24-25"

/tissue type="brain"

/clone_lib="Stratagene lambdaZap-II human fetal brain"

/dev_stage="fetal"

34. .1527

/function="inhibition of apoptosis"

/note="XIAP"

/codon_start=1

/evidence=experimental

/product="X-linked inhibitor of apoptosis protein"

/protein_id="AAC50373.1"

/db_xref="GI:1184320"

/translation="MTFNSFEGSKTCVTPADINKKEEFVEFNRLKTFANFPSPGSPVSA STLAGAGFLYTGEDTVRCFSCHAAVDWQYGDGSAVGRHRSKVPNCRFINGFYLENSA TQSTNSGIQNGQYKVENYLSRDHFDALDRPETHADYLLRTGQVVDISDTIYPRNPAM YCEEARLKSPQNPWDYAHLTRELASAGLYTIGIDQVQCFCGKLNWPCDRAWS EHRHFPNCFVLGRNLNIRSESDAVSSDRNPNSTNLPRNPSMADYEARIFTFGTWI YSVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDPEQHAQWYPGCKYLLEQK GQEIYNNHLTHSLEECVTEKTPSLTRRDDTIFQNMVQEAIRMGFSFKDIKKI MEKIQISGSNYKSLVLAQKDSMODSSQTSLOKEISTEEQLRRLQEEKLC KICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS"

108. .309

/note="encodes BIR1 (Baculovirus IAP Repeat)"

520. .723

/note="encodes BIR2"

826. .1020

/note="encodes BIR3"

1381. .1485

/note="encodes Ring Zinc Finger"

ORIGIN

Query Match 100.0%; Score 198; DB 9; Length 2540;

Best Local Similarity 100.0%; Pred. No. 2.6e-44;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 60

Db 826 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 945

QY 121 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 180

Db 946 GGAGGGCTAAGTGAAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGTTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198

Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 14

AX412131

LOCUS AX412131 3000 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 231 from Patent WO0226968.

ACCESSION AX412131

VERSION AX412131.1 GI:21444588

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.

TITLE Antisense iap nucleic acids and uses thereof

JOURNAL Patent: WO 0226968-A 231 04-APR-2002;

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers

source 1..3000

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 3000;

Best Local Similarity 100.0%; Pred. No. 2.5e-44;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 60

Db 1482 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 1541

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAAGTAAAGTGCTTTCACCTGTGGA 120

Db 1542 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAAGTAAAGTGCTTTCACCTGTGGA 1601

QY 121 GGAGGGCTAAGTATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180

Db 1602 GGAGGGCTAAGTATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1661

QY 181 CCAGGGTGCAAAATATCTG 198

Db 1662 CCAGGGTGCAAAATATCTG 1679

RESULT 15

AR106397

LOCUS

AR106397 5232 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 3 from patent US 6107041.

ACCESSION AR106397

VERSION AR106397.1 GI:12820927

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5232)

AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and

Pratt,C.

TITLE Detection and modulation of IAPS for the diagnosis and treatment of

proliferative disease

JOURNAL Patent: US 6107041-A 3 22-AUG-2000;

FEATURES Location/Qualifiers

source 1..5232

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 198; DB 6; Length 5232;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 60

Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAAGTAAAGTGCTTTCACCTGTGGA 120

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2004, 21:10:12 ; Search time 265 Seconds
(without alignments)
3174.125 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcagcgtctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: _geneseqn1990s:*
3: _geneseqn2000s:*
4: _geneseqn2001as:*
5: _geneseqn2001bs:*
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9: _geneseqn2003cs:*
10: _geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	198	100.0	1588	6	ABS52803 DNA encod
2	198	100.0	1659	3	Aaz48862 Human XIA
3	198	100.0	1659	7	ACA56455 Human sig
4	198	100.0	2404	6	Aak99405 DNA of AP
5	198	100.0	2540	2	Aat70836 Human apo
6	198	100.0	2540	3	Aaa64901 Human X-1
7	198	100.0	2540	6	ABK93869 Human CDN
8	198	100.0	2540	6	ABV94283 Breast ca
9	198	100.0	2540	7	AAL53731 X-linked
10	198	100.0	2540	7	AAD49663 Human X-1
11	198	100.0	2540	8	ADB81002 RING-SH C
12	198	100.0	3000	6	ABK93875 Human CDN
13	198	100.0	5232	2	AAV55038 Human XIA
14	180.4	91.1	1752	4	AAD03575 Human IAP
15	174.6	88.2	1988	2	AAT72710 Mouse inh
16	173	87.4	2100	2	AAT70839 Mouse apo
17	173	87.4	2100	6	ABK93872 Mouse CDN
18	169.8	85.8	2691	2	AAV55041 Murine XI
19	169.8	85.8	2691	7	ABZ58102 Mouse inh
20	166	83.8	711	4	AAD03582 Chimpanze
21	166	83.8	1758	6	ABK14678 Human inh
22	166	83.8	1758	6	ABK14677 Human inh
23	166	83.8	4993	4	AAD03581 Human IAP

24	164.4	83.0	711	3	AAA06940	Aaa06940 DNA encod
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26	164.4	83.0	1559	6	ABS52802	AbS52802 DNA encod
27	162.8	82.2	711	4	AAD03583	Aad03583 Gorilla I
28	157.8	79.7	578	2	AAX02960	Aax02960 Human IL-
29	131.4	66.4	802	2	AAX03018	Aax03018 Human IL-
30	96.8	48.9	302	6	ABQ58785	Abq58785 Human col
31	83	41.9	1402	2	AAx03028	Aax03028 Human IL-
32	78.6	39.7	2563	7	ACA56478	Aca56478 Human sig
33	78.6	39.7	2563	8	ADB80989	Adb80989 RING-SH C
34	78.6	39.7	2601	2	AAT61591	Aat61591 Human C-I
35	78.6	39.7	2666	2	AAT70837	Aat70837 Human apo
36	78.6	39.7	2676	6	ABK93870	Abk93870 Human CDN
37	78.6	39.7	3076	2	AAT72712	Aat72712 Human inh
38	78.6	39.7	3076	2	AAZ41005	Aaz41005 Human cel
39	78.6	39.7	3076	2	AAZ22096	Aaz22096 Human cel
40	78.6	39.7	3076	6	ABL62746	Ab162746 Breast ca
41	78.6	39.7	3076	6	ABL66325	Ab166325 Lung canc
42	78.6	39.7	3076	7	ABX10968	Abx10968 cDNA enco
43	78.6	39.7	3076	9	AAD60472	Aad60472 Human cel
44	78.6	39.7	3153	7	ABZ58104	Abz58104 Inhibitor
45	78.6	39.7	3164	7	ABV75363	Abv75363 Human CIA

ALIGNMENTS

RESULT 1
ABS52803
ID ABS52803 standard; DNA; 1588 BP.
XX
AC ABS52803;
XX
DT 15-NOV-2002 (first entry)
XX
DE DNA encoding X-linked inhibitor of apoptosis, XIAP.
XX
KW Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;
KW fertility; testicular cancer; male infertility; male birth control;
KW X-linked inhibitor of apoptosis; gene; ds.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT CDS 34..1527
FT /*tag= a
FT /transl_except= (pos:34..36, aa:Xaa)
FT /product= "X-linked inhibitor of apoptosis protein, XIAP"
FT /partial
FT /note= "Start codon illegible in specification;
represented as nnn"

US2002086409-A1.
04-JUL-2002.
18-DEC-2001; 2001US-00024433.
29-JAN-1998; 98US-0073001P.
29-JAN-1999; 99US-00239867.
(KORN/) KORNELUK R G.
(LAGA/) LAGACE M.
Korneluk RG, Lagace M;
WPI; 2002-642245/59.
P-PSDB; ABG32418.
Novel polypeptide, a member of inhibitor of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells, particular cells involved in male fertility.

PS Example 3; Fig 4A; 24pp; English.

XX A substantially pure XIAP polypeptide (I), a member of IAP (inhibitor of
CC apoptosis) family of proteins that is expressed in the testes. (I) is
CC useful for identifying a compound that modulates XIAP biological activity
CC (I) is useful for increasing apoptosis in a cell, preferably a germ-line
CC cell and for increasing fertility in an animal. (I) is useful for
CC treating or preventing apoptosis which occurs as a part of testicular
CC cancer and male infertility. XIAP may be manipulated for use as a male
CC birth control. XIAP polypeptides and nucleic acid sequences also have
CC diagnostic use in the detection or monitoring of conditions involving
CC aberrant levels of apoptosis. The present sequence represents the coding
CC sequence of X-linked inhibitor of apoptosis (XIAP)

XX SQ Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;

Query Match 100.0%; Score 198; DB 6; Length 1588;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 60
Db |||||
826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
Db |||||
886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db |||||
946 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db |||||
1006 CCAGGGTGCAAAATATCTG 1023

RESULT 2
AAZ48862
ID AAZ48862 standard; cDNA; 1659 BP.

XX AAZ48862;
AC
XX 24-MAR-2000 (first entry)
DT Human XIAP coding sequence.
XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta; ds.

XX Homo sapiens.
OS JP11326328-A.
PN 26-NOV-1999.
XX 13-MAY-1998; 98JP-00130378.
PF 13-MAY-1998; 98JP-00130378.
PR (MATS/), MATSUMOTO K.

XX WPI; 2000-078337/07.
DR P-PSDB; AAY59451.
XX Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein.
XX Disclosure; Page 28-30; 43pp; Japanese.

CC This sequence encodes the human XIAP protein. The invention relates to a
CC method for screening a substance inhibiting the formation of a complex
CC between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
CC (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding
CC protein 1 (TAB1) and a substance to be tested are contacted with each
CC other and then the presence or formation of a complex between XIAP and
CC TAB1 is detected. The substance can be used as a drug for extracellular
CC matrix protein production enhancement, cell growth inhibition, monocyte
CC migration, physiologically active substance induction, immunosuppression,
CC and beta-amyloid protein deposition. A substance inhibiting the formation
CC of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta
CC (Transforming growth factor-beta) type I and/or type II receptor is
CC useful as a drug

XX SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 3; Length 1659;
Best Local Similarity 100.0%; Pred. No. 3.1e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 60
Db |||||
874 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 933
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 120
Db |||||
934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACTGTGGA 993
QY 121 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db |||||
994 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053
QY 181 CCAGGGTGCAAAATATCTG 198
Db |||||
1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3
ACA56455
ID ACA56455 standard; cDNA; 1659 BP.

XX ACA56455;
AC
XX 06-JUN-2003 (first entry)
DT Human signalling pathway polynucleotide probe SEQ ID NO 1053.
XX Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX Homo sapiens.
OS US6500938-B1.
PN 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
PF 30-JAN-1998; 98US-00016434.
PR (INCY-) INCYTE GENOMICS INC.

XX Au-Young J, Seilhamer JJ;
PI WPI; 2003-352189/33.
XX Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX Claim 1; SEQ ID NO 1053; 65pp; English.

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1

SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
Query Match 100.0%; Score 198; DB 7; Length 1659;
Best Local Similarity 100.0%; Pred. No. 3.1e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAGGAGCAGCTT 60
Db 874 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAGGAGCAGCTT 933
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
Db 934 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 993
QY 121 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 994 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 4
AAK99405
ID AAK99405 standard; DNA; 2404 BP.
XX AAK99405;
AC AAK99405;
XX 27-JUN-2002 (first entry)
XX DNA of APP related human homologue hCP35211.
XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; gene; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 692..1528
FT /*tag= a
FT /product= "Protein of human homologue hCP35211"
FT /note= "No start codon"
XX WO200226820-A2.
PN
XX
XX 04-APR-2002.
PD
XX
XX 01-OCT-2001; 2001WO-EP011345.

XX 29-SEP-2000; 2000US-0236893P.
PR 14-JUN-2001; 2001US-0298309P.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWM, Zusman S;
XX WPI; 2002-315796/35.
DR P-PSDB; AAO20511.
XX New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease.
XX Example 4; Page 111; 129pp; English.
XX The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the APP related human homologue hCP35211
XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 6; Length 2404;
Best Local Similarity 100.0%; Pred. No. 3.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAGGAGCAGCTT 60
Db 827 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAGGAGCAGCTT 886
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
Db 887 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 946
QY 121 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 947 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1006
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1007 CCAGGGTGCAAAATATCTG 1024

RESULT 5
AAT70836
ID AAT70836 standard; cDNA; 2540 BP.
XX AAT70836;
AC AAT70836;
XX 02-SEP-1997 (first entry)
XX Human apoptosis inhibitor xiap cDNA.
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX Homo sapiens.
OS

XX Key Location/Qualifiers
FH CDS 34..1527
FT /*tag= a
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB001022.
XX
PF
XX 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
XX (UYOT-) UNIV OTTAWA.

XX Korneluk RG, Mackenzie AE, Baird S, Liston P;
PI
XX WPI; 1997-154262/14.
DR P-PSDB; AAW19581.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.

XX Claim 12; Page 67-68; 219pp; English.

XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
CC genes (AA70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
CC gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII
CC cDNA library using an X-linked sequence tag site that shows strong
CC homology with the conserved ring zinc finger domain of baculovirus CplAP
CC and OplAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
CC nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)

XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 6
AAA64901
ID AAA64901 standard; DNA; 2540 BP.
XX
AC AAA64901;

XX 07-NOV-2000 (first entry)

XX Human X-linked inhibitor of apoptosis DNA.

XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;

KW antiinflammatory; cytostatic; tumour; ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..1527
FT /*tag= a
FT /product= "X-linked inhibitor of apoptosis"

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-00392580.

XX 09-SEP-1999; 99US-00392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM, Ackermann EJ;

XX WPI; 2000-498201/44.

DR P-PSDB; AAY99985.

XX Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.

XX Example 13; Col 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to
PS inhibit expression of the human X-linked inhibitor of apoptosis. The
XX present sequence is the X-linked inhibitor of apoptosis DNA. Modified
CC phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more
CC effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
CC expression in cells and tissues in vitro. The oligonucleotides are also
CC useful for treating animals or humans, prone to a disease associated with
CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
CC prophylactically to prevent infection, inflammation or tumour formation

XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 3.6e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 7
ABK93869
ID ABK93869 standard; cDNA; 2540 BP.

XX ABK93869;

XX 26-AUG-2002 (first entry)

XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.

	Matches	198;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	TATGAAGCACGGATCTTTACTTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60 							
Dd	826	TATGAAGCACGGATCTTTACTTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	885 							
QY	61	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAGA TGCTTTTCAC TGTGGA	120 							
Dd	886	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAGA TGCTTTTCAC TGTGGA	945 							
QY	121	GGAGGGCTAAC TGATTGGAAGCC CAGTGAAGACC CT TTGGGAACA AC ATGC T AAAT GGTAT	180 							
Dd	946	GGAGGGCTAAC TGATTGGAAGCC CAGTGAAGACC CT TTGGGAACA AC ATGC T AAAT GGTAT	1005 							
QY	181	CCAGGGTGCAAATATCTG	198 							
Dd	1006	CCAGGGTGCAAATATCTG	1023 							

RESULT 11	
ADB81002	
ID	ADB81002 standard; DNA; 2540 BP.
XX	
AC	ADB81002;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	RING-SH complex related DNA, SEQ ID No 76.
XX	
KW	RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60;
KW	Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsG101;
KW	cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
KW	rhabdovirus; filovirus; gene; ds.
XX	
OS	Unidentified.
XX	
PN	WO2003033646-A2.
XX	
PD	24-APR-2003.
XX	
PF	31-JUL-2002; 2002WO-US024589.
XX	
PR	31-JUL-2001; 2001US-0308958P.
PR	09-NOV-2001; 2001US-0345846P.
XX	
PA	(PROT-) PROTEOLOGICS INC.
XX	
PI	Greener T, Moskowitz H, Reiss Y, Alroy I;
XX	
DR	WPI; 2003-393509/37.
DR	P-PSDB; ADB80961.
XX	
PT	New isolated protein complex comprising a RING-SH 3 polypeptide and
PT	another polypeptide, useful for detecting cells infected with a virus,
PT	and for treating viral disorders caused by retroviruses, rhabdoviruses,
PT	or filoviruses.
XX	
PS	Disclosure; Fig 75; 176pp; English.
XX	
CC	The invention relates to a novel isolated protein complex comprising a
CC	RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
CC	Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
CC	STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsG101, a cullin, RING-SH, and a
CC	clathrin. The novel protein complex has virucide activity and can be used
CC	to treat disorders as part of a vaccine. The protein complex and
CC	composition are useful for detecting cells infected with a virus, for
CC	identifying agents having antiviral activity, and for treating viral
CC	disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
CC	polynucleotide represents a DNA sequence relating to a protein comprising
CC	the RING-SH complex of the invention.
XX	
SO	Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 8; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 3.6e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60
Db	826	TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	885
QY	61	GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGA	120
Db	886	GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGA	945
QY	121	GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT	180
Db	946	GGAGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT	1005
QY	181	CCAGGGTGCAAAATATCTG	198
Db	1006	CCAGGGTGCAAAATATCTG	1023

RESULT 12
 ABK93875
 ID ABK93875 standard; cDNA; 3000 BP.
 XX
 AC ABK93875;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.
 XX
 KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 FN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOF-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI; 2002-479562/51.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX
 PS Example 2; Fig 15; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,

PI Duckett C, Mir SS;
XX WPI; 2001-258135/26.
DR P-PSDB; AAE00359.
XX
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis.
XX
XX Claim 18; Page 87-88; 108pp; English.
PS
XX
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-3
CC (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14. ILP-3
CC comprises a spacer region and a ring finger domain. The ILP-3 interacts
CC with transforming growth factor beta receptor (TGFbetaR) and modulates
CC TGFbetaR activity. ILP-3 also moderately inhibits ILP-1 mediated c-Jun N-
CC terminal kinase (JNK) activation when co-transfected with ILP-1. Such
CC activity decreases or prevents apoptosis in a cell. ILP-3 is used in the
CC area of genetic testing for predisposition to diseases, such as
CC osteoarthritis, hypothyroidism, juvenile nephronophthisis, thrombophilia,
CC colorectal cancer and neonatal purpura fulminans owing to an ILP-3
CC deletion or mutation. The ILP-3 is also used in the treatment of diseases
CC associated with abnormal apoptosis such as cancer, autoimmune diseases,
CC e.g., diabetes and multiple sclerosis and neurodegenerative diseases
CC including retinal degeneration. The ILP-3 gene is also used in gene
CC therapy for treating patients suffering from ILP-3 gene deletions or
CC mutations
XX
SQ Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 U; 0 Other;

Query Match 91.1%; Score 180.4; DB 4; Length 1752;
Best Local Similarity 94.4%; Pred. No. 1.8e-48;
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 499 TATGAAGCAGGATCTTTACTTTTGGGATGTGGATATATTCAGTTAAACAAGGAGCAGCTT 558
|||||
QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
Db 559 TCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 618
|||||
QY 121 GGAGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 619 GGGGGCTAACTGATTGGAAGCCCGAGCGAAGACCCCTTGGGAACAACATGATAAATGGCAT 678
|||||
QY 181 CCAGGCTGCAAAATATCTG 198
|||||
Db 679 CCAGGCTGTAATATCTG 696
|||||

RESULT 15
AAT72710
ID AAT72710 standard; DNA; 1988 BP.
XX
AC AAT72710;
XX
DT 16-SEP-1997 (first entry)
XX
DE Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
KW degenerative disease; infectious disease; autoimmune disease; cancer;
KW gene therapy; diagnosis; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 212..1702
FT /*tag= a
XX
PN WO9723501-A1.

XX 03-JUL-1997.
XX
XX 20-DEC-1996; 96WO-AU0000827.
XX
XX 22-DEC-1995; 95AU-00007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI; 1997-350966/32.
DR P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
PT modulate apoptosis for treatment of degenerative, infectious or
PT auto-immune diseases and cancer.
XX
XX Claim 24; Page 44-47; 136pp; English.
PS
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
CC homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver
CC cDNA library on the basis of homology to Orgyia pseudotsuguta
CC polyhedrosis virus IAP BIR and RING finger amino acid motifs. Animal IAP
CC homologue nucleic acids (see also AAT72711-17) can be used to produce
CC polypeptides useful in methods for modulating apoptosis in animal cells,
CC specifically for treatment, by inhibition, of degenerative and infectious
CC disease or, by promotion, of cancer and autoimmune disease, and can be
CC used for gene therapy of these diseases
XX
SQ Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other;

Query Match 88.2%; Score 174.6; DB 2; Length 1988;
Best Local Similarity 92.9%; Pred. No. 1.4e-46;
Matches 183; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1001 TATGAAGCAGGATCGTTACTTTTGGAAACATGGACATCCTCAGTTAAACAAGGAGCAGCTT 1060
|||||
QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
Db 1061 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTGAAGTCTTCACTGTGGA 1120
|||||
QY 121 GGAGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 1121 GGAGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCGAAGTGTAT 1180
|||||
QY 181 CCAGGCTGCAAAATATCT 197
|||||
Db 1181 CCAGGCTGCAAAATACCT 1197
|||||

Search completed: March 13, 2004, 04:35:13
Job time : 270 secs

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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:07:08 ; Search time 62 Seconds
(without alignments)
1772.263 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcagcgatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	100.0	1588	4	US-09-239-867-3
2	198	100.0	1659	4	US-09-016-434-1053
3	198	100.0	2540	2	US-08-511-485-3
4	198	100.0	2540	3	US-09-392-580-1
5	198	100.0	2540	4	US-09-201-936-3
6	198	100.0	2540	4	US-09-023-655-900
7	198	100.0	2540	4	US-09-011-356-3
8	198	100.0	2540	4	US-09-672-717-218
9	198	100.0	3000	4	US-09-672-717-231
10	198	100.0	5232	3	US-09-212-971-3
11	198	100.0	5232	3	US-08-800-929A-3
12	198	100.0	5232	4	US-09-617-053A-3
13	173	87.4	2100	2	US-08-511-485-9
14	173	87.4	2100	4	US-09-201-936-9
15	173	87.4	2100	4	US-09-011-356-9
16	173	87.4	2100	4	US-09-672-717-224
17	169.8	85.8	2691	3	US-09-212-971-9
18	169.8	85.8	2691	3	US-08-800-929A-9
19	169.8	85.8	2691	4	US-09-617-053A-9
20	164.4	83.0	711	3	US-09-121-979-3
21	164.4	83.0	711	3	US-09-332-319-3
22	164.4	83.0	1559	4	US-09-239-867-1
23	157.8	79.7	152331	3	US-09-128-155-16
24	131.4	66.4	176373	3	US-09-128-155-17
25	78.6	39.7	2563	4	US-09-016-434-1076
26	78.6	39.7	2563	4	US-09-023-655-894
27	78.6	39.7	2601	3	US-08-569-749-3

28	78.6	39.7	2601	5	PCT-US96-12860-3
29	78.6	39.7	2676	2	US-08-511-485-5
30	78.6	39.7	2676	4	US-09-201-936-5
31	78.6	39.7	2676	4	US-09-011-356-5
32	78.6	39.7	2676	4	US-09-672-717-220
33	78.6	39.7	3076	2	US-09-205-144-1
34	78.6	39.7	6669	3	US-09-212-971-5
35	78.6	39.7	6669	3	US-08-800-929A-5
36	78.6	39.7	6669	4	US-09-617-053A-5
37	78.6	39.7	6669	4	US-09-672-717-230
38	74.4	37.6	1435	5	PCT-US95-05922A-1
39	74.4	37.6	2580	2	US-08-511-485-7
40	74.4	37.6	2580	4	US-09-201-936-7
41	74.4	37.6	2580	4	US-09-011-356-7
42	74.4	37.6	2580	4	US-09-672-717-222
43	74.4	37.6	2589	3	US-08-569-749-1
44	74.4	37.6	2589	5	PCT-US96-12860-1
45	74.4	37.6	3532	2	US-09-205-204-1

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match 100.0%; Score 198; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 2
US-09-016-434-1053
; Sequence 1053, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

;; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;; NUMBER OF SEQUENCES: 1490
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016,434
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0002 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1053:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1659 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g1016687
;; US-09-016-434-1053

Query Match 100.0%; Score 198; DB 4; Length 1659;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 874 TATGAGCAGCGGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 933

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 120
Db 934 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 993

QY 121 GGAGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 994 GGAGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 3
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/511,485
;; FILING DATE: 04-AUG-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 07540/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2540 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: DNA (genomic)
;; US-08-511-485-3

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAGCAGCGGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGCTAACTGATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 4
US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRE
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)

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US-09-392-580-1
Query Match      100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTAAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTAAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023
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RESULT 5
US-09-201-936-3
; Sequence 3, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3
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Query Match      100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
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QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 6
US-09-023-655-900
; Sequence 900, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENE BANK
; CLONE: g1184319
US-09-023-655-900
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Query Match      100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTCTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGTGAATAAGTCTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023
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RESULT 10
US-09-212-971-3
; Sequence 3, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)...(4623)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4622)...(4622)
; OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 11
US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF

; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 60
DB 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
DB 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 12
US-09-617-053A-3
; Sequence 3, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
NAME/KEY: variation
LOCATION: (4622)...(4622)
OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3

Query Match 100.0%; Score 198; DB 4; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 13
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485

FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 87.4%; Score 173; DB 2; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATATCTCAGTTAACAAGGAGCAGCTT 60
Db 916 TATGAAGCACGGATCTTTACTTTTGGAAACATGGATATATCTCAGTTAACAAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 976 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 1035

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db 1036 GGAGGCTCACTGATTGGAAGCCAGTGAAGACCCCTTGGGACCAGCATGCTAAGTGCTAC 1095

QY 181 CCAGGGTGCAAAATATCT 197
Db 1096 CCAGGGTGCAAAATACCT 1112

RESULT 14
US-09-201-936-9
; Sequence 9, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 87.4%; Score 173; DB 4; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY      61  GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 120
Db      976  GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGA 1035

QY      121  GGAGGGCTAACTGATTGGAGGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db      1036 GGAGGGCTCAGCGATTGGAGGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1095

QY      181  CCAGGGTGCAAAATATCT 197
Db      1096 CCAGGGTGCAAAATACCT 1112
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US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-011-356-9
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Query Match      87.4%; Score 173; DB 4; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      1  TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db      916 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 975

QY      61  GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTTTCACTGTGGA 120
Db      976  GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGA 1035

QY      121  GGAGGGCTAACTGATTGGAAGGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db      1036 GGAGGGCTCAGCGATTGGAGGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1095

QY      181  CCAGGGTGCAAAATATCT 197
Db      1096 CCAGGGTGCAAAATACCT 1112
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Search completed: March 13, 2004, 06:26:51
Job time : 64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:27:28 ; Search time 207 Seconds
(without alignments)
3521.528 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcaggtattttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 1840798884 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09E_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	100.0	1659	15	US-10-305-720-1053 Sequence 1053, Ap
2	198	100.0	2404	9	US-09-964-899-38 Sequence 38, Appli
3	198	100.0	2540	9	US-09-201-936-3 Sequence 3, Appli
4	198	100.0	2540	14	US-10-007-926A-274 Sequence 274, App
5	198	100.0	5232	9	US-09-974-592-3 Sequence 3, Appli
6	173	87.4	2100	9	US-09-201-936-9 Sequence 9, Appli
7	169.8	85.8	2691	9	US-09-974-592-9 Sequence 9, Appli
8	157.8	79.7	152331	13	US-10-095-407-16 Sequence 16, Appli
9	131.4	66.4	176373	13	US-10-095-407-17 Sequence 17, Appli
10	78.6	39.7	255	14	US-10-102-524-906 Sequence 906, App
11	78.6	39.7	2563	15	US-10-305-720-1076 Sequence 1076, Ap
12	78.6	39.7	2601	14	US-10-232-286-3 Sequence 3, Appli
13	78.6	39.7	2676	9	US-09-201-936-5 Sequence 5, Appli
14	78.6	39.7	2916	12	US-10-240-425-1436 Sequence 1436, Ap
15	78.6	39.7	3076	9	US-09-954-456-1635 Sequence 1635, Ap

16	78.6	39.7	3076	9	US-09-954-531-16 Sequence 16, Appli
17	78.6	39.7	3076	14	US-10-197-290-1 Sequence 1, Appli
18	78.6	39.7	3076	15	US-10-388-263-157 Sequence 157, App
19	78.6	39.7	3164	14	US-10-141-618-5 Sequence 5, Appli
20	78.6	39.7	3165	14	US-10-269-909-5 Sequence 5, Appli
21	78.6	39.7	3734	14	US-10-353-461-7 Sequence 7, Appli
22	78.6	39.7	5844	10	US-09-971-392-253 Sequence 253, App
23	78.6	39.7	5857	14	US-10-247-671-18 Sequence 18, Appli
24	78.6	39.7	6669	9	US-09-974-592-5 Sequence 5, Appli
25	74.4	37.6	1435	8	US-08-464-588-1 Sequence 1, Appli
26	74.4	37.6	1435	14	US-10-323-643-1 Sequence 1, Appli
27	74.4	37.6	2531	14	US-10-207-655-199 Sequence 199, App
28	74.4	37.6	2580	9	US-09-201-936-7 Sequence 7, Appli
29	74.4	37.6	2589	14	US-10-232-286-1 Sequence 1, Appli
30	74.4	37.6	3496	14	US-10-153-668-337 Sequence 337, App
31	74.4	37.6	3532	9	US-09-880-107-3354 Sequence 3354, Ap
32	74.4	37.6	3532	15	US-10-464-158-1 Sequence 1, Appli
33	74.4	37.6	3732	9	US-09-974-592-7 Sequence 7, Appli
34	74.4	37.6	4614	10	US-09-814-353-19934 Sequence 19934, A
35	71.2	36.0	2862	14	US-10-232-286-13 Sequence 13, Appli
36	71.2	36.0	3151	9	US-09-974-592-13 Sequence 13, Appli
37	71	35.9	7990	14	US-10-311-455-131 Sequence 7, Appli
38	71	35.9	7990	14	US-10-240-452-7 Sequence 11, Appli
39	70.6	35.7	2676	9	US-09-974-592-11 Sequence 41, Appli
40	69.6	35.2	2416	9	US-09-201-936-41 Sequence 39, Appli
41	69	34.8	2450	9	US-09-201-936-39 Sequence 1, Appli
42	59	29.8	3773	14	US-10-041-859-1 Sequence 132, App
43	56.6	28.6	7990	14	US-10-311-455-132 Sequence 8, Appli
44	56.6	28.6	7990	14	US-10-240-452-8 Sequence 1, Appli
45	54.6	27.6	5504	8	US-08-913-322-1

ALIGNMENTS

RESULT 1

US-10-305-720-1053
; Sequence 1053, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1053
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1016687
US-10-305-720-1053

Query Match	100.0%;	Score 198;	DB 15;	Length 1659;
Best Local Similarity	100.0%;	Pred. No. 5.9e-55;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCAGTTAACAGGACAGCTT	60	
Db	874	TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCAGTTAACAGGACAGCTT	933	
QY	61	GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTCTTTTCACTGTGGA	120	
Db	934	GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAAGTCTTTTCACTGTGGA	993	
QY	121	GGAGGGCTAACTGATTGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT	180	
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
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; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)..(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

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: GENERAL INFORMATION:
: APPLICANT: Cohen, Dalia et al.
: TITLE OF INVENTION: Identification of Genes Involved in
: TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanocaster

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; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53

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; SOFTWARE: FastSEQ for Windows Version 4.0

SEO ID NO 38

; LENGTH: 2404

: TYPE: DNA

ORGANISM: Homo Sapien

US-09-964-899-38

Query Match	100.0%;	Score 198;	DB 9;	Length 2404;
Best Local Similarity	100.0%;	Pred. No. 7e-55;		
Matches 198:	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

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QY	61	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTTCACGTGTGGA	120
DB	887	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTTCACGTGTGGA	946
QY	121	GGAGGGCTAACTGATTGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT	180
DB	847	GGAGGGCTAACTGATTGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT	1006

Qy 181 CCAGGGTGCAAATATCTG 198
Db 1007 CCAGGGTGCAAATATCTG 1024

RESULT 3
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45

RESULT 4

US-10-007-926A-274
: Sequence 274. Application US/10007926A

Publication No. US20030143539A1

: GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCO

APPLICANT: HOUTGATTE, REMI

APPLICANT: DANIEL BITENBAIN; AFFILIANT: HOEGH, KONG

APPLICANT: NGIVEN CATH

APPLICANT: NOUÏEN, CATHERINE
APPLICANT: VIENS, PATRICIA

APPLICANT: VIENS, FAIRICE
APPLICANT: FEET VINCENT

APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRI

THE LITTLE FOETUS

FILE OF INVENTION: USING ANGLES OF CIRCLES
FILE REFERENCE: 1546-P-00

FILE REFERENCE: 1348-K-00
CURRENT APPLICATION NUMBER: IIS/1

; CURRENT APPLICATION NUMBER: US/10/00
- CURRENT FILING DATE: 2001-12-07

CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/

;; PRIOR APPLICATION NUMBER: 3000-12-

;; PRIOR FILING DATE: 2000-12-
: NUMBER OF SEQ ID NOS: 468

; NUMBER OF SE SOFTWARE: DE

; SOFTWARE: FAL
CFO ID NO 374; SEQ ID NO 2
1 ENCELI.; LENGTH: 2540
TYPE: DATA

; TYPE: DN

ORGANISM: Homo sapiens

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;
FEATURE:
CUTTER INFORMATION:

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OTHER INFORMATION

US-10-007-926A-274

Query Match	100.0%;	Score 198;	DB 14;	Length 2540;
Best Local Similarity	100.0%;	Pred. No. 7.2e-55;		
Matches 198;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

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Db	886	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA	945

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db |||||||
QY 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
Db |||||||
QY 181 CCAGGGTGCAAAATATCTG 198
Db |||||||
1006 CCAGGGTGCAAAATATCTG 1023

RESULT 5
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

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Best Local Similarity 100.0%; Pred. No. 1e-54;
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QY 61 GCAAGAGCTGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACCTGGGA 120
Db |||||||
886 GCAAGAGCTGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACCTGGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db |||||||
946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db |||||||
1006 CCAGGGTGCAAAATATCTG 1023

RESULT 6
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9
Query Match 87.4%; Score 173; DB 9; Length 2100;
Best Local Similarity 92.4%; Pred. No. 1.2e-46;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db |||||||
916 TATGAAGCAGGATCGTTACTTTTGGGAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 975
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACCTGTGGA 120
Db |||||||
976 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACCTGTGGA 1035
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
Db |||||||
1036 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGACCCCTTGGGACCAGCATGCTAAAGTGTAC 1095
QY 181 CCAGGGTGCAAAATATCT 197
Db |||||||
1096 CCAGGGTGCAAAATACCT 1112

RESULT 7
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Db 163 CAAATGCTTTTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 104

Qy 162 ACAACATGCTAAATGGTATCCAGGGTGCAATATCTG 198

Db 103 TCAACATGCCAAGTGGTTTCCCAAGGTGTGAGTACTTG 67

RESULT 11

US-10-305-720-1076

Sequence 1076, Application US/10305720

Publication No. US20040010136A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

FILE REFERENCE: PA-0002-1 CON

CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: 09/016,434

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1076

LENGTH: 2563

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: GenBank ID No. US20040010136A1 g1160974

US-10-305-720-1076

Query Match 39.7%; Score 78.6; DB 15; Length 2563;

Best Local Similarity 68.8%; Pred. No. 2.3e-15;

Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGT 101

Db 932 AGTTAATCCTGAGCAGCTTGCAAGTGCGGGTTTTATTATTATGTGGTAACAGTGATGATGT 991

Qy 102 AAAGTGCTTTCACTGTGGAGAGGGCTAACTGATTTGGAGCCCAAGACCCCTTGGGA 161

Db 992 CAAATGCTTTTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1051

Qy 162 ACAACATGCTAAATGGTATCCAGGGTGCAATATCTG 198

Db 1052 TCAACATGCCAAGTGGTTTCCCAAGGTGTGAGTACTTG 1088

RESULT 12

US-10-232-286-3

Sequence 3, Application US/10232286

Publication No. US20030143579A1

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

Goedel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,286

FILING DATE: 30-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2601 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-232-286-3

Query Match 39.7%; Score 78.6; DB 14; Length 2601;

Best Local Similarity 68.8%; Pred. No. 2.4e-15;

Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 42 AGTTAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGT 101

Db 932 AGTTAATCCTGAGCAGCTTGCAAGTGCGGGTTTTATTATTATGTGGTAACAGTGATGATGT 991

Qy 102 AAAGTGCTTTCACTGTGGAGAGGGCTAACTGATTTGGAGCCCAAGACCCCTTGGGA 161

Db 992 CAAATGCTTTTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1051

Qy 162 ACAACATGCTAAATGGTATCCAGGGTGCAATATCTG 198

Db 1052 TCAACATGCCAAGTGGTTTCCCAAGGTGTGAGTACTTG 1088

RESULT 13

US-09-201-936-5

Sequence 5, Application US/09201936

Publication No. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES, AND DETECTION METHODS

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: PCT/IB96/01022

EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-12-22

EARLIER APPLICATION NUMBER: 08/511,485

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 2676

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (2470)...(2470)

OTHER INFORMATION: N may be any nucleotide

FEATURE:

NAME/KEY: variation

LOCATION: (2476)...(2476)

OTHER INFORMATION: N may be any nucleotide

FEATURE:

NAME/KEY: variation
LOCATION: (2483)...(2483)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2602)...(2602)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 39.7%; Score 78.6; DB 9; Length 2676;
Best Local Similarity 68.8%; Pred. No. 2.4e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 42 AGTTAAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGT 101
Db 998 AGTTAATCCTGAGCAGCTTGCAAGAGTGGGGTTTTATTATGTTGGTTAAACAGTGAATGAT 1057
QY 102 AAAGTGCTTTCACTGTGGAGGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTTGGGA 161
Db 1058 CAAATGCTTTTCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 1117
QY 162 ACAACATGCTAAATGGTATCCAGGGTGCATAATATCTG 198
Db 1118 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 1154

RESULT 14
US-10-240-425-1436
Sequence 1436, Application US/10240425
Publication No. US20040033502A1
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Bolland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1436
LENGTH: 2916
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 U45878
NAME/KEY: unsure
LOCATION: (1)..(2907)
OTHER INFORMATION: n = a or c or g or t
US-10-240-425-1436

Query Match 39.7%; Score 78.6; DB 12; Length 2916;
Best Local Similarity 68.8%; Pred. No. 2.5e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 42 AGTTAAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGT 101
Db 1258 AGTTAATCCTGAGCAGCTTGCAAGTGGGGTTTTATTATGTTGGTTAAACAGTGAATGAT 1317
QY 102 AAAGTGCTTTCACTGTGGAGGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTTGGGA 161
Db 1318 CAAATGCTTTTCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 1377
QY 162 ACAACATGCTAAATGGTATCCAGGGTGCATAATATCTG 198

Db 1378 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 1414

RESULT 15
US-09-954-456-1635
Sequence 1635, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1635
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 39.7%; Score 78.6; DB 9; Length 3076;
Best Local Similarity 68.8%; Pred. No. 2.5e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 42 AGTTAAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGT 101
Db 1534 AGTTAATCCTGAGCAGCTTGCAAGTGGGGTTTTATTATGTTGGTTAAACAGTGAATGAT 1593
QY 102 AAAGTGCTTTCACTGTGGAGGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTTGGGA 161
Db 1594 CAAATGCTTTTCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 1653
QY 162 ACAACATGCTAAATGGTATCCAGGGTGCATAATATCTG 198
Db 1654 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 1690

Search completed: March 13, 2004, 06:34:00
Job time : 210 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:02:03 ; Search time 2177.5 Seconds
(without alignments)
2715.367 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcacggatctttac.....atccagggtgcaaatatctg 198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	83.8	1805	11 BC039318	BC039318 Homo sapi
2	166	83.8	1851	11 BC056914	BC056914 Homo sapi
3	164.6	83.1	773	14 CD350778	CD350778 UI-M-G10-
4	164.4	83.0	1789	11 BC046168	BC046168 Homo sapi

C	5	157.4	79.5	628	9	AI573382	AI573382 mn83e12.x
	6	114	57.6	1177	12	BM805359	BM805359 AGENCOURT
	7	112	56.6	536	9	AUI23207	AUI23207 AUI23207
	8	104.4	52.7	716	9	AV706807	AV706807 AV706807
C	9	100.2	50.6	318	10	BF659610	BF659610 uz88e12.x
	10	99	50.0	617	10	BB663325	BB663325 BB663325
C	11	96.4	48.7	721	29	CE100865	CE100865 tigr-gss-
	12	94.4	47.7	504	10	BB650856	BB650856 BB650856
C	13	91.6	46.3	334	12	BM220130	BM220130 C0935E08-
	14	91.6	46.3	584	13	BQ552032	BQ552032 H4013A06-
C	15	90.8	45.9	791	14	CF222542	CF222542 AGENCOURT
	16	87	43.9	420	28	AQ011995	AQ011995 HS_2190_A
C	17	85	42.9	1494	29	AY398943	AY398943 Homo sapi
	18	84	42.4	849	28	BZ242580	BZ242580 CH230-252
	19	80.6	40.7	373	13	BY662508	BY662508 BY662508
	20	79.4	40.1	663	13	BU658508	BU658508 cl37a11.2
	21	78.6	39.7	341	10	AW375598	AW375598 QV0-CT017
	22	78.6	39.7	354	10	AW375594	AW375594 QV0-CT017
	23	78.6	39.7	402	10	AW846507	AW846507 QV0-CT017
	24	78.6	39.7	531	10	AW375599	AW375599 QV0-CT017
	25	78.6	39.7	532	10	AW846425	AW846425 QV0-CT017
	26	78.6	39.7	546	10	AW846421	AW846421 QV0-CT017
	27	78.6	39.7	571	10	AW375649	AW375649 QV0-CT017
C	28	78.6	39.7	582	10	AW846337	AW846337 QV0-CT017
	29	78.6	39.7	590	10	BE268377	BE268377 601124994
	30	78.6	39.7	621	10	AW375648	AW375648 QV0-CT017
	31	78.6	39.7	680	10	AW375625	AW375625 QV0-CT017
	32	78.6	39.7	886	13	BQ652590	BQ652590 AGENCOURT
	33	78.6	39.7	1472	29	AY398945	AY398945 Mus muscu
	34	78.6	39.7	1799	29	AY420753	AY420753 Homo sapi
	35	78.4	39.6	269	10	BE506790	BE506790 db87g08.y
	36	74.4	37.6	441	12	BM312708	BM312708 ig78a10.y
C	37	74.4	37.6	563	9	AA702174	AA702174 zi91g08.s
	38	74.4	37.6	652	9	AV704923	AV704923 AV704923
	39	74.4	37.6	831	13	BU935186	BU935186 AGENCOURT
	40	74.4	37.6	851	12	BI253303	BI253303 602973538
	41	74.4	37.6	896	13	BQ439248	BQ439248 AGENCOURT
	42	74.4	37.6	917	13	BU928804	BU928804 AGENCOURT
	43	74.4	37.6	1084	13	BU902159	BU902159 AGENCOURT
	44	74.2	37.5	690	29	CE697566	CE697566 tigr-gss-
	45	74	37.4	354	9	AA354707	AA354707 EST63004

ALIGNMENTS

RESULT 1	BC039318	BC039318	1805 bp	mrna	linear	HTC 18-NOV-2002
LOCUS	Homo sapiens	Similar to baculoviral IAP repeat-containing 8, clone IMAGE:5269405, mRNA.				
DEFINITION	BC039318	BC039318.1	GI:25058167			
ACCESSION	BC039318	HTC.				
VERSION	BC039318	Homo sapiens (human)				
KEYWORDS	HTC.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1805)				
AUTHORS	Strausberg,R.					
TITLE	Direct Submission					
JOURNAL	Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov					
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome					

RESULT 3
CD350778 773 bp mRNA linear EST 09-JUL-2003
LOCUS UI-M-GIO-cgh-g-23-0-UI.r1 NIH_BMAP_GIO Mus musculus cDNA clone
DEFINITION IMAGE:6853392 5', mRNA sequence.
CD350778
ACCESSION CD350778.1 GI:31142365
VERSION
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 773)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
FEATURES
Location/Qualifiers
1..773
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6853392"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GIO"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Query Match 83.1%; Score 164.6; DB 14; Length 773;
Best Local Similarity 92.5%; Pred. No. 5.7e-40;
Matches 173; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 11 GGATCTTTACTTTGGACATGGATATATCTCAGTTAAACAAGGAGCAGCTTGCAAGAGCTG 70
|||||
Db 1 GGATCGTTACTTTTGGAACATGGACATCCTCAGTTAAACAAGGAGCAGCTTGCAAGAGCTG 60
71 GATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTTCACTGTGGAGGAGGGCTAA 130
|||||
QY 61 GATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTTTCACTGTGGAGGAGGGCTCA 120
131 CTGATTGGAAGCCAGTGGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCA 190
|||||
QY 121 CGGATTGGAAGCCAAAGTGAAGACCCCTTGGGAACAGCATGCGAAGTGTGTACCCAGGGTGCA 180
191 AATATCT 197
|||||

Db 181 AATACCT 187
RESULT 4
BC046168 1789 bp mRNA linear HTC 13-FEB-2003
LOCUS Homo sapiens, similar to baculoviral IAP repeat-containing 8, clone
DEFINITION IMAGE:5742590, mRNA.
ACCESSION BC046168
VERSION BC046168.1 GI:28374455
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1789)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (31-JAN-2003) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library preparation: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 107 Row: i Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: frame shifted.
FEATURES
Location/Qualifiers
1..1789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742590"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
ORIGIN
Query Match 83.0%; Score 164.4; DB 11; Length 1789;
Best Local Similarity 89.4%; Pred. No. 9.4e-40;
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 TATGAAGCACCGGATCTTTACTTTTGGGACATGGATATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1002 TATGAAGCCCGGCTCATTTACTTTTGGGACATGGATGTTCTCCGTCAACAAGAGCAGCTT 1061
61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
|||||
QY 1062 GCAAGAGCTGGATTTTATGCTATAGGTCAAGAGGATAAAGTACAGTCTTTCACTGTGGA 1121
121 GGAGGGCTAACTGATTTGGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
QY 1122 GGAGGGCTAGCCCACTGGAGGCCCAAGGAAGATCCTTGGGAACAGCATGCTAAATGGTAT 1181
181 CCAGGGTGCAAAATATCTG 198
|||||
Db 1182 CCAGGTTGCAAAATATCTG 1199

RESULT 5
AI573382/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
QY
Db
QY
Db
QY
Db
QY
Db
RESULT 6
BM805359
LOCUS

AI573382
mn83e12.x1
IMAGE:550702 3'
AI573382
AI573382.1
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 628)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 440.
Location/Qualifiers
1. .628
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGCGACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

628 bp mRNA linear EST 16-APR-1999
Tcell 937311 Mus musculus cDNA clone
TR:Q60989 Q60989 MIHA. i, mRNA sequence.
GI:4536756
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 628)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 440.
Location/Qualifiers
1. .628
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGCGACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

79.5%; Score 157.4; DB 9; Length 628;
90.4%; Pred. No. 8.9e-38;
0; Mismatches 18; Indels 1; Gaps 1;
1 TATGAAGCACGGATCTTTACTTTTGGACATGGATATACCTCAGTTAACAGGAGCAGCTT 60
|||||
604 TATGAAGCACGGATCGTTACTTTTGGNACATGGACATCCTCAGTTACAAAGGAGCAGCTT 545
|||||

61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
544 GCAAGAGCT-GATTTTATGCTTTAGTTGAAGGCGATAAAGTGAAGTCTTCACTGTGGA 486
|||||

121 GGAGGGCTAACTGATTTGAAGCCCGAGTGAAGACCCCTTGGGAACCAACATGCTAAATGGTAT 180
|||||
485 GGAGGGCTACCGGATTTGAAGCCCAAGTGAAGACCCCTTGGGAACCAAGCATGCGAAGTGGTAC 426
|||||

181 CCAGGGTGCAAAATATCT 197
|||||
425 NCAGGGTGCAAAATACCT 409
|||||

BM805359 1177 bp mRNA linear EST 05-MAR-2002

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
QY
Db
RESULT 7
AUI23207
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AGENCOURT_6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
5', mRNA sequence.
BM805359
BM805359.1 GI:19122182
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.
Location/Qualifiers
1. .1177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5728685"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

57.6%; Score 114; DB 12; Length 1177;
100.0%; Pred. No. 3.1e-24;
0; Mismatches 0; Indels 0; Gaps 0;
114; Conservative 0;
85 GGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTGATGGAAGCCC 144
|||||
142 GGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTGATGGAAGCCC 201
|||||

145 AGTGAAGACCCCTTGGGAACCAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 198
|||||
202 AGTGAAGACCCCTTGGGAACCAACATGCTAAATGGTATCCAGGGTGCAAAATATCTG 255
|||||

536 bp mRNA linear EST 01-AUG-2002
NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
sequence.
AUI23207
AUI23207.1 GI:10947923
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 536)
Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y., Ishii, S., Saito, K.,
Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y.,
Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)

JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES Location/Qualifiers
source 1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"
ORIGIN
Query Match 56.6%; Score 112; DB 9; Length 536;
Best Local Similarity 98.2%; Pred. No. 9.4e-24;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
|||||
Db 99 GGTGAAGGTGATAAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAACTGATTGGAAGCCC 158
QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTGCAATATCTG 198
|||||
Db 159 AGTGAANACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTGCAATATCTG 212
AV706807 716 bp mRNA linear EST 09-OCT-2000
LOCUS AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.
DEFINITION AV706807
ACCESSION AV706807
VERSION AV706807.1 GI:10724085
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
TITLE Homo sapiens cDNA ADB clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADBCOF01"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"

/clone_lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Query Match 52.7%; Score 104.4; DB 9; Length 716;
Best Local Similarity 94.7%; Pred. No. 2.4e-21;
Matches 108; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
|||||
Db 156 GGTGAAGGTGATAAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAACTGATTGGAAGCCC 215
QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTGCAATATCTG 198
|||||
Db 216 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTGCAATATCTG 269
RESULT 9
BF659610/c 318 bp mRNA linear EST 29-DEC-2000
LOCUS BF659610 NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:3676174 3,
DEFINITION similar to SW: IAP3_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3 ; ,
mRNA sequence.
ACCESSION BF659610
VERSION BF659610.1 GI:11924744
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 318)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-rc@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1436942
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 226.
FEATURES Location/Qualifiers
source 1..318
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3676174"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
ORIGIN
Query Match 50.6%; Score 100.2; DB 10; Length 318;
Best Local Similarity 92.9%; Pred. No. 3.4e-20;
Matches 105; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 53 AGCAGCTTGCAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTC 112
|||||

COMMENT		Other_ESTs: H4013A06-5 Contact: Yong Qian Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4013 row: A column: 06 Seq primer: -21M13 Forward High quality sequence stop: 584 POLYA=Yes.	
FEATURES		Location/Qualifiers	
source		1. .584 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6" /db_xref="niaEST:H4013A06-3" /db_xref="taxon:10090" /clone="H4013A06" /sex="mixed" /dev_stage="mixed" /lab_host="DH10B" /clone_lib="NIA Mouse 7.4K cDNA Clone Set" /note="Vector: pSPORT1; Site_1: Sali; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."	
ORIGIN		Query Match 46.3%; Score 91.6; DB 13; Length 584; Best Local Similarity 91.5%; Pred. No. 2e-17; Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
QY	82	TTAGGTGAAGTGATAAAGTAAGTAAAGTCTTTTCTACTGTGGAGGAGGGCTAACTGATTGGAAG	141
Db	260	TTAGGTGAAGGCGATAAAGTGAAGTCTTTTCTACTGTGGAGGAGGGCTACCGATTGGAAG	201
QY	142	CCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTATCCAGGGT	187
Db	200	CCAAGTGAAGACCCCTTGGGAACACATGCGAAGTGTGTTACCCAGGGT	155
RESULT 15		CF222542 791 bp mRNA linear EST 04-AUG-2003	
LOCUS		AGENCOURT_14926978 NICHD_XGC_Emb5 Silurana tropicalis cDNA clone	
DEFINITION		IMAGE:6981334 5', mRNA sequence.	
ACCESSION		CF222542	
VERSION		CF222542.1 GI:33423250	
KEYWORDS		EST.	
SOURCE		Silurana tropicalis (western clawed frog) Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana. 1 (bases 1 to 791) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Robert M. Grainger cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14642 row: f column: 21 High quality sequence start: 3	
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			

COMMENT		Other_ESTs: H4013A06-5 Contact: Yong Qian Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4013 row: A column: 06 Seq primer: -21M13 Forward High quality sequence stop: 584 POLYA=Yes.	
FEATURES		Location/Qualifiers	
source		1. .584 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6" /db_xref="niaEST:H4013A06-3" /db_xref="taxon:10090" /clone="H4013A06" /sex="mixed" /dev_stage="mixed" /lab_host="DH10B" /clone_lib="NIA Mouse 7.4K cDNA Clone Set" /note="Vector: pSPORT1; Site_1: Sali; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."	
ORIGIN		Query Match 46.3%; Score 91.6; DB 13; Length 584; Best Local Similarity 91.5%; Pred. No. 2e-17; Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
QY	82	TTAGGTGAAGTGATAAAGTAAGTAAAGTCTTTTCTACTGTGGAGGAGGGCTAACTGATTGGAAG	141
Db	260	TTAGGTGAAGGCGATAAAGTGAAGTCTTTTCTACTGTGGAGGAGGGCTACCGATTGGAAG	201
QY	142	CCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTATCCAGGGT	187
Db	200	CCAAGTGAAGACCCCTTGGGAACACATGCGAAGTGTGTTACCCAGGGT	155
RESULT 15		CF222542 791 bp mRNA linear EST 04-AUG-2003	
LOCUS		AGENCOURT_14926978 NICHD_XGC_Emb5 Silurana tropicalis cDNA clone	
DEFINITION		IMAGE:6981334 5', mRNA sequence.	
ACCESSION		CF222542	
VERSION		CF222542.1 GI:33423250	
KEYWORDS		EST.	
SOURCE		Silurana tropicalis (western clawed frog) Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana. 1 (bases 1 to 791) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Robert M. Grainger cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14642 row: f column: 21 High quality sequence start: 3	
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			

ORIGIN

Search completed: March 13, 2004, 06:24:39
Job time : 2184.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 13, 2004, 00:37:57 ; Search time 1045.5 Seconds
(without alignments)
8208.437 Million cell updates/sec

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcagcagtgattac.....accagggtgcaaataccta 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	2100	6	AR302739	AR302739 Sequence
2	198	100.0	2100	6	AR435474	AR435474 Sequence
3	198	100.0	2100	6	AX412124	AX412124 Sequence
4	194.8	98.4	2691	6	AR106400	AR106400 Sequence
5	194.8	98.4	2691	6	AR116702	AR116702 Sequence
6	194.8	98.4	2691	6	AR370620	AR370620 Sequence
7	194.8	98.4	2691	6	AX670906	AX670906 Sequence
8	194.8	98.4	2691	6	BD190871	BD190871 Detection
9	194.8	98.4	2691	10	MMU88990	U88990 Mus musculu
10	186.8	94.3	1988	10	MMU36842	U36842 Mus muscu
11	185.2	93.5	205991	2	AC109227	AC109227 Mus muscu
12	185.2	93.5	208236	2	AC137152	AC137152 Mus muscu
13	182	91.9	1491	10	AF183429	AF183429 Rattus no
14	182	91.9	2468	10	AB033366	AB033366 Rattus no
15	182	91.9	3032	10	AF304334	AF304334 Rattus no
16	180.4	91.1	2032	10	AF304333	AF304333 Rattus no
17	173	87.4	1588	6	AR263641	AR263641 Sequence
18	173	87.4	1659	6	E31042	E31042 Method for
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21	173	87.4	2086	9	BC032729	BC032729 Homo sapi
22	173	87.4	2404	6	AX429575	AX429575 Sequence
23	173	87.4	2540	6	AR103281	AR103281 Sequence
24	173	87.4	2540	6	AR302736	AR302736 Sequence
25	173	87.4	2540	6	AR380355	AR380355 Sequence
26	173	87.4	2540	6	AR435471	AR435471 Sequence
27	173	87.4	2540	6	AX412118	AX412118 Sequence
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29	173	87.4	2540	9	HSU45880	U45880 Human X-lin
30	173	87.4	3000	6	AX412131	AX412131 Sequence
31	173	87.4	5232	6	AR106397	AR106397 Sequence
32	173	87.4	5232	6	AR116699	AR116699 Sequence
33	173	87.4	5232	6	AR370617	AR370617 Sequence
34	173	87.4	5232	6	AX670900	AX670900 Sequence
35	173	87.4	5232	6	BD190868	BD190868 Detection
36	157	79.3	1752	6	AX104956	AX104956 Sequence
37	157	79.3	1752	9	AF164681	AF164681 Homo sapi
38	157	79.3	154214	9	AC079753	AC079753 Homo sapi
39	149	75.3	1758	6	AX370787	AX370787 Sequence
40	149	75.3	1758	6	AX370789	AX370789 Sequence
41	149	75.3	4993	6	AX104968	AX104968 Sequence
42	149	75.3	4993	9	AF164682	AF164682 Homo sapi
43	149	75.3	144301	9	AC010467	AC010467 Homo sapi
44	149	75.3	165662	9	AC092070	AC092070 Homo sapi
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ALIGNMENTS

RESULT 1
AR302739
LOCUS AR302739 2100 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9 from patent US 6541457.
ACCESSION AR302739
VERSION AR302739.1 GI:31691182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian IAP gene family, primers, probes and detection methods
JOURNAL Patent: US 6541457-A 9 01-APR-2003;
FEATURES Location/Qualifiers

source 1. .2100
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 60
Db 916 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 975
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Db 1036 GGAGGGCTCAGCGATTTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113
RESULT 2
AR435474
LOCUS AR435474 2100 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6656704.
ACCESSION AR435474
VERSION AR435474.1 GI:40198325
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Baird,S. and Liston,P.
TITLE Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
JOURNAL Patent: US 6656704-A 9 02-DEC-2003;
FEATURES Location/Qualifiers
source 1. .2100
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 198; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 60
Db 916 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 975
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Db 976 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCAGCGATTTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 180
Db 1036 GGAGGGCTCAGCGATTTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113
RESULT 3
AX412124
LOCUS AX412124 2100 bp DNA linear PAT 15-JUN-2002
DEFINITION Sequence 224 from Patent WO0226968.
ACCESSION AX412124

VERSION AX412124.1 GI:21444584
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 224 04-APR-2002;
FEATURES University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
Location/Qualifiers
source 1. .2100
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Query Match 100.0%; Score 198; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 60
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Db 1036 GGAGGGCTCAGCGATTTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113
RESULT 4
AR106400
LOCUS AR106400 2691 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107041.
ACCESSION AR106400
VERSION AR106400.1 GI:12820930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
source 1. .2691
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAACAGGAGCAGCTT 60
Db 1461 TATGAAGCACGGATCGTTACTTTTGGAAACATGGACATCCTCAGTTAACAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580

QY 121 GGAGGGCTCAGGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 5
AR116702
LOCUS AR116702 2691 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6133437.
ACCESSION AR116702
VERSION AR116702.1 GI:14097024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..2691
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Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
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QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 7
AX670906 2691 bp DNA linear PAT 27-MAR-2003
LOCUS AX670906
DEFINITION Sequence 9 from Patent EP1277836.
ACCESSION AX670906
VERSION AX670906.1 GI:29329409
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and Pratt,C.
TITLE Modulation of the iaps and naip for the treatment of proliferative diseases
JOURNAL Patent: EP 1277836-A 9 22-JAN-2003;
FEATURES Location/Qualifiers
source 1..2691
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Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
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QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 8
BD190871
LOCUS BD190871 2691 bp DNA linear PAT 17-JUL-2003
DEFINITION Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease.
ACCESSION BD190871

Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580

QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 7
AX670906 2691 bp DNA linear PAT 27-MAR-2003
LOCUS AX670906
DEFINITION Sequence 9 from Patent EP1277836.
ACCESSION AX670906
VERSION AX670906.1 GI:29329409
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and Pratt,C.
TITLE Modulation of the iaps and naip for the treatment of proliferative diseases
JOURNAL Patent: EP 1277836-A 9 22-JAN-2003;
FEATURES Location/Qualifiers
source 1..2691
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ORIGIN
Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
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QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGCTAC 180
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QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 8
BD190871
LOCUS BD190871 2691 bp DNA linear PAT 17-JUL-2003
DEFINITION Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease.
ACCESSION BD190871

VERSION BD190871.1 GI:33000610
KEYWORDS JP 2002512602-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and Pratt,C.
TITLE Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease
JOURNAL Patent: JP 2002512602-A 4 23-APR-2002;
COMMENT UNIVERSITY OF OTTAWA
PN JP 2002512602-A/4
PD 23-APR-2002
PF 13-FEB-1998 JP 1998531325
PR 13-FEB-1997 US 08/800929
PI ROBERT KORNELUK,ALEXANDER E MACKENZIE,PETER LISTON,STEPHEN PI BAIRD,
PI BENJAMIN TSANG,CHRISTINE PRATT
PC A61K38/17,A61K31/70,A61K39/395,C12N15/11,C12Q1/68,G01N33/50,
PC G01N33/574,
PC A01K67/027,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Query Match 98.4%; Score 194.8; DB 6; Length 2691;
Best Local Similarity 99.0%; Pred.No.1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCACGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
Db 1461 TATGAAGCACGATCGTTACTTTTGGAAACATGGATATCTCCTCAGTTAAACAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
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QY 121 GGAGGGCTCACGATTTGGAAGCCAGCAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCACGATTTGGAAGCCAGCAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 1640
QY 181 CCAGGGTGCAATACCTA 198
Db 1641 CCAGGGTGCAATACCTA 1658
RESULT 9
MMU88990
LOCUS
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA,
complete cds.
ACCESSION U88990
VERSION U88990.1 GI:2138318
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2691)
AUTHORS Farahani,R., Lefebvre,C., Korneluk,R.G. and MacKenzie,A.E.
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani,R., Lefebvre,C., Korneluk,R.G. and MacKenzie,A.E.
TITLE Direct Submission

JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES
source
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STLARAGFLYTGEQTVQCFSCAAIDRWQYGDSDAVGRHRRISPNCRFINGFYFENGA
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SVNKEQLARAGFYALGEDKVKCFHCGGLTDWKPSEDPDQHAHCYKPGCKYLLDEKG
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1646..1724
/gene="miap-3"
/number=3
1725..1767
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1768..1968
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Query Match 98.4%; Score 194.8; DB 10; Length 2691;
Best Local Similarity 99.0%; Pred.No.1e-44;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCACGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCACGATTTGGAAGCCAGCAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCACGATTTGGAAGCCAGCAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 1640
QY 181 CCAGGGTGCAATACCTA 198
Db 1641 CCAGGGTGCAATACCTA 1658
RESULT 10
MMU36842
LOCUS
DEFINITION Mus musculus IAP homolog A (MIHA) mRNA, complete cds.

ACCESSION U36842
VERSION U36842.1 GI:1145260
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1988)
AUTHORS Uren,A.G., Pakusch,M., Hawkins,C.J., Puls,K.L. and Vaux,D.L.
TITLE Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE 96209843
PUBMED 8643514
REFERENCE 2 (bases 1 to 1988)
AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall Institute, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES
source Location/Qualifiers
1. 1988
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57 Black 6 x CBA"
/db_xref="taxon:10090"
/sex="female"
/tissue_type="liver"
/dev_stage="6-8 weeks old"
1. 1988
/gene="MIHA"
212. 1702
/gene="MIHA"
/note="apoptosis inhibitor; homolog of Baculovirus IAP protein"
/codon_start=1
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/db_xref="GI:1145261"
/translation="MTFNSFEGTRTFVLADTNKDEEFVEFNRLKTFANFPSSPVSA
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misc_feature 1556. 1660
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/note="RING finger"
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Query Match 94.3%; Score 186.8; DB 10; Length 1988;
Best Local Similarity 96.5%; Pred. No. 2e-42;
Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCGCTT 60
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QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
Db |
1061 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCACTGTGGA 1120

QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db |
1121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGAAACAGCATGCGAAGTGGTAC 1180
QY 181 CCAGGGTGCAAAATACCTA 198
Db |
1181 CCAGGGTGCAAAATACCTA 1198
RESULT 11
AC109227
LOCUS Mus musculus clone RP23-396C19, WORKING DRAFT SEQUENCE, 8 unordered
DEFINITION pieces.
ACCESSION AC109227
VERSION AC109227.4 GI:28475838
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205991)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-396C19
Unpublished
2 (bases 1 to 205991)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 205991)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
JOURNAL Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Feb 24, 2003 this sequence version replaced gi:28269624. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20802
Center clone name: 396_C_19
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 202609 bases at least Q40
Consensus quality: 203944 bases at least Q30
Consensus quality: 204698 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 205291; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-fp
Quality coverage: 8.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 42349: contig of 42349 bp in length
* 42350 42449: gap of 100 bp
* 42450 44657: contig of 2208 bp in length
* 44658 44757: gap of 100 bp
* 44758 51328: contig of 6571 bp in length
* 51329 51428: gap of 100 bp
* 51429 62775: contig of 11347 bp in length
* 62776 62875: gap of 100 bp
* 62876 71924: contig of 9049 bp in length
* 71925 72024: gap of 100 bp
* 72025 185178: contig of 113154 bp in length
* 185179 185278: gap of 100 bp
* 185279 203699: contig of 18421 bp in length
* 203700 203799: gap of 100 bp
* 203800 205991: contig of 2192 bp in length.
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185279..203699
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clone_end:r7
vector_side:right"
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Best Local Similarity 96.0%; Pred. No. 2.6e-42;
Matches 190; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
Db 43490 TATGAAGCACGGGTCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 43549
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTCCACTGTGGA 120
Db 43550 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCCTCCACTGTGGA 43609
QY 121 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 43610 GGAGGGCTCACGGTTTGAAGCCCAAGTGAAGATCCTGGGACCAGCATGCTAAGTGCTAT 43669
QY 181 CCAGGGTGCAAAATACCTA 198
Db 43670 CCAGGGTGTAATATCTA 43687
RESULT 12
AC137152/c
LOCUS AC137152 208236 bp DNA linear HTG 27-NOV-2002
DEFINITION Mus musculus chromosome UNK clone RP24-269A16, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
AC137152
AC137152.1 GI:25054276
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 208236)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 208236)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 208236)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0269A16
----- Summary Statistics -----
Sequencing vector: M13; %
Sequencing vector: plasmid; %
Chemistry: Dye-primer ET; % of reads
Chemistry: Dye-terminator Big Dye; % of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 200615 bases at least Q40
Consensus quality: 202070 bases at least Q30
Consensus quality: 203024 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 4713 6345: contig of 1633 bp in length
* 6346 7770: contig of 1325 bp in length
* 7771 7870: gap of unknown length
* 7871 9368: contig of 1498 bp in length
* 9369 9468: gap of unknown length
* 9469 11493: contig of 2025 bp in length
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* 11594 13278: contig of 1685 bp in length
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* 17338 17437: gap of unknown length
* 17438 22936: contig of 5499 bp in length
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* 34823 34922: gap of unknown length
* 34923 43533: contig of 8611 bp in length
* 43534 43633: gap of unknown length
* 43634 66136: contig of 22503 bp in length
* 66137 66236: gap of unknown length
* 66237 85245: contig of 19009 bp in length
* 85246 85345: gap of unknown length
* 85346 106030: contig of 20685 bp in length
* 106031 106130: gap of unknown length
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FEATURES

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Location/Qualifiers

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/chromosome="UNK"
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1382. .2667
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2768. .4612
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4713. .6345
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6446. .7770
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7871. .9368
/note="assembly_name:Contig19"
9469. .11493
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11594. .13278
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13379. .17337
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17438. .22936
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ORIGIN

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Best Local Similarity 96.0%; Pred. No. 2.6e-42;
Matches 190; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAAGGAGCAGCTT 60
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Db 195106 TATGAAGCACGGGTCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAAGGAGCAGCTT 195047
Qy 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
|||||
Db 195046 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTTCACCTGTGGA 194987
Qy 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTCTAC 180
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Db 194986 GGAGGGCTCAGGTTTGGGAAGCCCAAGTGAAGATCCTGGGACCAGCATGCTAAGTGTCTAT 194927
Qy 181 CCAGGGTGCAAAATACCTA 198
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Db 194926 CCAGGGTGTAATATCTA 194909

RESULT 13

AF183429

LOCUS AF183429 1491 bp mRNA linear ROD 16-JUL-2002

DEFINITION Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete

cds.

ACCESSION AF183429

VERSION AF183429.1 GI:10765280

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 1491)

AUTHORS Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.

TITLE Cloning and characterization of the rat homologues of the Inhibitor

of Apoptosis protein 1, 2, and 3 genes

JOURNAL BMC Genomics 3 (1), 5 (2002)

PUBMED 11860601

REFERENCE 2 (bases 1 to 1491)

AUTHORS Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology

and Immunology, University of Ottawa, 451 Smyth Road, Ottawa,

Ontario K1H 8M5, Canada

FEATURES Location/Qualifiers

source

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/mol_type="mRNA"

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ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 1491;
Best Local Similarity 94.9%; Pred. No. 4.9e-41;
Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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Db 910 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAT 969
181 CCAGGGTGCAAAATACCTA 198
970 CCAGGGTGTAATATCTA 987

RESULT 14

AB033366
LOCUS AB033366 2468 bp mRNA linear ROD 15-OCT-1999
DEFINITION Rattus norvegicus riap3 mRNA, complete cds.
ACCESSION AB033366
VERSION AB033366.1 GI:6045147
KEYWORDS RIAP3.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 2468)
Saito,N.
AUTHORS Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA
TITLE Published Only in DataBase (1999)
JOURNAL
REFERENCE 2 (bases 1 to 2468)
Saito,N.
AUTHORS Direct Submission
TITLE Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo,
JOURNAL Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655,
Japan (E-mail:nsaito-tky@umin.ac.jp, Tel: +81-3-5800-8853,
Fax: +81-3-5800-8655)
Location/Qualifiers

FEATURES

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/db_xref="taxon:10116"
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CSEEARLKTQNPWDYAHLSPRELASAGLYYTIGIDDQVQFCGCGKLKNWPCDRAWS
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gene

CDS

ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 2468;
Best Local Similarity 94.9%; Pred. No. 4.5e-41;
Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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Db 1239 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAT 1298
181 CCAGGGTGCAAAATACCTA 198
1299 CCAGGGTGTAATATCTA 1316

RESULT 15

AF304334
LOCUS AF304334 3032 bp mRNA linear ROD 21-MAY-2003
DEFINITION Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA,
complete cds.
ACCESSION AF304334
VERSION AF304334.1 GI:11890720
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3032)
Lareu,R.R., Lacher,M.D., Bradley,C.K., Sridaran,R., Friis,R.R. and
AUTHORS Dharmarajan,A.M.
TITLE Regulated expression of inhibitor of apoptosis protein 3 in the rat
corpus luteum
JOURNAL Biol. Reprod. 68 (6), 2232-2240 (2003)
MEDLINE 22642584
PUBMED 12606402
REFERENCE 2 (bases 1 to 3032)
Lareu,R.R., Lacher,M., Friis,R.R. and Dharmarajan,A.M.
AUTHORS Direct Submission
TITLE Submitted (08-SEP-2000) Anatomy and Human Biology, University of
JOURNAL Western Australia, Verdum St, Nedlands, WA 6907, Australia
Location/Qualifiers

FEATURES

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/db_xref="taxon:10116"
/clone="2"
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926. .2431
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/protein_id="AAG41193.1"
/db_xref="GI:11890721"

CDS

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CSEEARLKTQNPWDYAHLSPRELASAGLYYTIGIDDQVQFCGCGKLKNWPCDRAWS
EHRHFPNCFVFLGNVNRVSESGVSDRNFPNSTNPRNPAMAEYDARIIVTFTGLY
SVNKEQLARAGFYALGEDKVKCFHCGGLTDWKPSEDWEQHAQWYPCGKYLLDEKG
QEVNNIHLTHSLGESVVRTAECTPSVTKKIDDTIFQNPVMQEAIRMGFNFKDIKKT

BEKLTSGSNYSLEVLJADLVSAQKDNSQDESSQTSIQKDI STEEQLRRLQBEKLCCK
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ORIGIN

Query Match 91.9%; Score 182; DB 10; Length 3032;
Best Local Similarity 94.9%; Pred. No. 4.3e-41;
Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY	61	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA	120
Db	1775	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTGAAGTGTCTTTCACCTGTGGA	1834
QY	121	GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTAC	180
Db	1835	GGAGGGCTCAGCGATTGGAGCCAAAGTGAAGACCCCTTGGGAACAGCATGCTAAGTGTAT	1894
QY	181	CCAGGGTGCAAAATACCTA	198
Db	1895	CCAGGGTGTAATATCTA	1912

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Job time : 1046.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2004, 21:10:12 ; Search time 265 Seconds
(without alignments)
3174.125 Million cell updates/sec

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcagcgatcggttac.....acccagggtgcaataaccta 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	198	100.0	2100	2	AAT70839
2	198	100.0	2100	6	ABK93872
3	194.8	98.4	2691	2	AAV55041
4	194.8	98.4	2691	7	ABZ58102
5	186.8	94.3	1988	2	AAT72710
6	173	87.4	1588	6	ABS52803
7	173	87.4	1659	3	AAZ48862
8	173	87.4	1659	7	ACA56455
9	173	87.4	2404	6	AAK99405
10	173	87.4	2540	2	AAT70836
11	173	87.4	2540	3	AAA64901
12	173	87.4	2540	6	ABK93869
13	173	87.4	2540	6	ABV94283
14	173	87.4	2540	7	AAL53731
15	173	87.4	2540	7	AAD49663
16	173	87.4	2540	8	ADB81002
17	173	87.4	3000	6	ABK93875
18	173	87.4	5232	2	AAV55038
19	157	79.3	1752	4	AAD03575
20	149	75.3	1758	6	ABK14678
21	149	75.3	1758	6	ABK14677
22	149	75.3	4993	4	AAD03581
23	147.4	74.4	711	3	AAA06940

24	147.4	74.4	1559	6	ABK13197	Abk13197 Human tes
25	147.4	74.4	1559	6	ABS52802	AbS52802 DNA encod
26	145.8	73.6	711	4	AAD03582	Aad03582 Chimpanze
27	144.2	72.8	711	4	AAD03583	Aad03583 Gorilla I
28	134.4	67.9	578	2	AAx02960	Aax02960 Human IL-
29	109.6	55.4	802	2	AAx03018	Aax03018 Human IL-
30	79.8	40.3	1402	2	AAx03028	Aax03028 Human IL-
31	77.8	39.3	302	6	ABQ58785	Abq58785 Human col
32	76	38.4	2563	7	ACA56478	Aca56478 Human sig
33	76	38.4	2563	8	ADB80989	Adb80989 RING-SH C
34	76	38.4	2601	2	AAT61591	Aat61591 Human c-I
35	76	38.4	2666	2	AAT70837	Aat70837 Human apo
36	76	38.4	2676	6	ABK93870	Abk93870 Human cdn
37	76	38.4	3076	2	AAT72712	Aat72712 Human inh
38	76	38.4	3076	2	AAZ41005	Aaz41005 Human cel
39	76	38.4	3076	2	AAZ22096	Aaz22096 Human cel
40	76	38.4	3076	6	ABL62746	Ab162746 Breast ca
41	76	38.4	3076	6	ABL66325	Ab166325 Lung canc
42	76	38.4	3076	7	ABX10968	Abx10968 CDNA enco
43	76	38.4	3076	9	AAD60472	Aad60472 Human cel
44	76	38.4	3153	7	ABZ58104	Abz58104 Inhibitor
45	76	38.4	3164	7	ABV75363	Abv75363 Human CIA

ALIGNMENTS

RESULT 1
AAT70839
ID AAT70839 standard; cDNA; 2100 BP.
XX
AC AAT70839;
XX
DT 02-SEP-1997 (first entry)
XX
DE Mouse apoptosis inhibitor m-xiap cDNA.
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP;
KW HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 127..1617
FT /*tag= a
XX
FN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB001022.
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX
DR WPI; 1997-154262/14.
DR P-PSDB; AAW19584.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
PS Claim 11; Page 78-79; 219pp; English.
XX
CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
CC genes (AAT70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The murine

CC xiap gene (for X-linked IAP gene) sequence was constructed from 12
CC overlapping clones isolated from a mouse embryo lambda-gt11 cDNA library
CC and from a mouse FIX II genomic library using human xiap cDNA as probe.
CC IAP nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)
XX
SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
916 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
976 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 1035

QY 121 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1036 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 1095

QY 181 CCAGGGTGCAAAATACCTA 198
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1096 CCAGGGTGCAAAATACCTA 1113

RESULT 2
ABK93872
ID ABK93872 standard; cDNA; 2100 BP.
XX
AC ABK93872;
XX
DT 26-AUG-2002 (first entry)
XX
DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
XX
KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytotstatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Mus sp.
XX
XX WO200226968-A2.
PN
XX 04-APR-2002.
PD
XX 27-SEP-2001; 2001WO-CA001379.
PF
XX 28-SEP-2000; 2000US-00672717.
PR
XX (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
PI
XX WPI; 2002-479562/51.
DR
XX P-PSDB; ABG65666.
DR
XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.
XX
XX Disclosure; Fig 4; 135pp; English.
PS
XX The invention relates to an inhibitor of apoptosis (IAP) antisense

CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC cDNA sequence
XX
SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;

Query Match 100.0%; Score 198; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
916 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
976 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 1035

QY 121 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1036 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCAGCATGCTAAGTGCTAC 1095

QY 181 CCAGGGTGCAAAATACCTA 198
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1096 CCAGGGTGCAAAATACCTA 1113

RESULT 3
AAV55041
ID AAV55041 standard; cDNA; 2691 BP.
XX
XX AAV55041;
AC
XX 13-NOV-1998 (first entry)
DT
XX Murine XIAP coding sequence.
DE
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
KW
XX Mus sp.
OS
XX
FH Key Location/Qualifiers
FT CDS 672..2162
FT /*tag= a
FT /product= "XIAP"
XX
XX WO9835693-A2.
PN
XX 20-AUG-1998.
PD
XX 13-FEB-1998; 98WO-IB0000781.
PF
XX 13-FEB-1997; 97US-00800929.
PR
XX (UYOT-) UNIV OTTAWA.
PA
XX Korneluk R, Mackenzie AE, Liston P, Baird S, Tsang B, Pratt C;
PI
XX

DR WPI; 1998-467164/40.
DR P-PSDB; AAW69297.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP
PT or NAIP polypeptide - also methods for prognosis based on presence of IAP
PT and NAIP, specifically applied to cancers involving p53 mutations.
XX
PS Claim 13; Fig 4; 147pp; English.
XX
CC This sequence encodes the mouse XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors
XX
SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;
Query Match 98.4%; Score 194.8; DB 2; Length 2691;
Best Local Similarity 99.0%; Pred. No. 2.8e-57;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAACAAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCAGCGATTGGAGACCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGCGATTGGAGACCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658
RESULT 4
ABZ58102
ID ABZ58102 standard; cDNA; 2691 BP.
XX
AC ABZ58102;
XX
DT 22-APR-2003 (first entry)
XX
DE Mouse inhibitor of apoptosis protein MIAP3 cDNA.
XX
KW Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
KW lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy;
KW gene; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 672..2162
FT /*tag= a
FT /product= "MIAP3"
XX
XX WO2003004606-A2.
PN
PD 16-JAN-2003.
XX

PF 03-JUL-2002; 2002WO-US021002.
XX
PR 03-JUL-2001; 2001US-00898158.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Troy CM, Shelanski ML;
XX
DR WPI; 2003-210351/20.
DR P-PSDB; ABP72157.
XX
PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for
PT treating cancer, neurodegenerative disorder or cardiomyopathy.
XX
PS Disclosure; Fig 15B; 124pp; English.
XX
CC The present sequence is that of cDNA encoding murine inhibitor of
CC apoptosis protein MIAP3. The invention provides a nucleic acid, such as
CC an antisense oligonucleotide, which specifically hybridises to a nucleic
CC acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2,
CC MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's
CC death comprises contacting the cell with the nucleic acid under
CC conditions permitting the nucleic acid to enter the cell, especially the
CC use of a vector, liposome, or a mechanical or electrical means. The
CC method is used to treat acute lymphocytic leukaemia, acute myelogenous
CC leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer,
CC lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal
CC cell carcinoma and squamous cell carcinoma (all claimed)
XX
SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;
Query Match 98.4%; Score 194.8; DB 7; Length 2691;
Best Local Similarity 99.0%; Pred. No. 2.8e-57;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAACAAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCAGCGATTGGAGACCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGCGATTGGAGACCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658
RESULT 5
AAT72710
ID AAT72710 standard; DNA; 1988 BP.
XX
AC AAT72710;
XX
DT 16-SEP-1997 (first entry)
XX
DE Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
KW degenerative disease; infectious disease; autoimmune disease; cancer;
KW gene therapy; diagnosis; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
CDS 212..1702
FT /*tag= a
XX
PN WO9723501-A1.

XX 03-JUL-1997.
XX 20-DEC-1996; 96WO-AU0000827.
XX 22-DEC-1995; 95AU-00007275.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Vaux DL;
XX WPI; 1997-350966/32.
XX P-PSDB; AAW19745.
XX Isolated protein homologues of viral inhibitors of apoptosis - used to
XX modulate apoptosis for treatment of degenerative, infectious or
XX auto-immune diseases and cancer.
XX Claim 24; Page 44-47; 136pp; English.
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver
XX cDNA library on the basis of homology to Orgyia pseudotsuguta
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs. Animal IAP
XX homologue nucleic acids (see also AAT72711-17) can be used to produce
XX polypeptides useful in methods for modulating apoptosis in animal cells,
XX specifically for treatment, by inhibition, of degenerative and infectious
XX disease or, by promotion, of cancer and autoimmune disease, and can be
XX used for gene therapy of these diseases
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other;
XX Query Match 94.3%; Score 186.8; DB 2; Length 1988;
XX Best Local Similarity 96.5%; Pred. No. 1.6e-54;
XX Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
Db |||||
1001 TATGAAGCAGCGATCGTTACTTTTGGACATGGACATCCTCAGTTAACAAGGAGCAGCTT 1060
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db |||||
1061 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1120
QY 121 GGAGGGCTCAGGATTGGAGSCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTAC 180
Db |||||
1121 GGAGGGCTCAGGATTGGAGSCAAGTGAAGACCCCTGGGACCAGCATGCGAAGTGTAC 1180
QY 181 CCAGGGTGCAAAATACCTA 198
Db |||||
1181 CCAGGGTGCAAAATACCTA 1198
RESULT 6
ABS52803
ID ABS52803 standard; DNA; 1588 BP.
XX
AC ABS52803;
XX
DT 15-NOV-2002 (first entry)
XX
DE DNA encoding X-linked inhibitor of apoptosis, XIAP.
XX
KW Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP;
XX fertility; testicular cancer; male infertility; male birth control;
XX X-linked inhibitor of apoptosis; gene; ds.
XX Mammalia.
XX
FH Key Location/Qualifiers
FT CDS 34..1527
/*tag= a

FT /transl_except= (pos:34..36, aa:Xaa)
FT /product= "X-linked inhibitor of apoptosis protein, XIAP"
FT /partial
FT /note= "Start codon illegible in specification;
XX represented as nnn"
PN US2002086409-A1.
XX
XX 04-JUL-2002.
XX
XX 18-DEC-2001; 2001US-00024433.
XX
XX 29-JAN-1998; 98US-0073001P.
XX 29-JAN-1999; 99US-00239867.
XX (KORN/) KORNELUK R G.
XX (LAGA/) LAGACE M.
XX
XX Korneluk RG, Lagace M;
XX
XX WPI; 2002-642245/69.
XX P-PSDB; ABG32418.
XX
XX Novel polypeptide, a member of inhibitor of apoptosis family of proteins
XX that is expressed in testes useful for modulating apoptosis in cells,
XX particular cells involved in male fertility.
XX Example 3; Fig 4A; 24pp; English.
XX A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of
XX apoptosis) family of proteins that is expressed in the testes. (I) is
XX useful for identifying a compound that modulates TIAP biological activity
XX (I) is useful for increasing apoptosis in a cell, preferably a germ-line
XX cell and for increasing fertility in an animal. (I) is useful for
XX treating or preventing apoptosis which occurs as a part of testicular
XX cancer and male infertility. TIAP may be manipulated for use as a male
XX birth control. TIAP polypeptides and nucleic acid sequences also have
XX diagnostic use in the detection or monitoring of conditions involving
XX aberrant levels of apoptosis. The present sequence represents the coding
XX sequence of X-linked inhibitor of apoptosis (XIAP)
SQ Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
Query Match 87.4%; Score 173; DB 6; Length 1588;
Best Local Similarity 92.4%; Pred. No. 9.4e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
Db |||||
826 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db |||||
886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTGGAGSCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTAC 180
Db |||||
946 GGAGGGCTAAGTGAAGTGAAGCCAGTGAAGACCCCTTGGGAACAACAATGATGAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db |||||
1006 CCAGGGTGCAAAATATCT 1022
RESULT 7
AAZ48862
ID AAZ48862 standard; cDNA; 1659 BP.
XX
AC AAZ48862;
XX
DT 24-MAR-2000 (first entry)
XX
DE Human XIAP coding sequence.

RESULT 9
AAK99405
ID AAK99405 standard; DNA; 2404 BP.
XX
AC AAK99405;
XX
DT 27-JUN-2002 (first entry)
XX
DE DNA of APP related human homologue hCP35211.
XX
KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 692..1528
FT /*tag= a
FT /product= "Protein of human homologue hCP35211"
FT /note= "No start codon"
XX
PN WO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP011345.
XX
PR 29-SEP-2000; 2000US-0236893P.
PR 14-JUN-2001; 2001US-0298309P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWHM, Zusman S;
XX
DR WPI; 2002-315796/35.
XX
PT New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease.
XX
PS Example 4; Page 111; 129pp; English.
XX
CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the APP related human homologue hCP35211
XX
SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 6; Length 2404;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
Dd 827 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 886
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120

Dd 887 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTATAAAGTAAAGTCTTCACTGTGGA 946
QY 121 GGAGGGCTCACGATTTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGTAAGTGCTAC 180
Dd 947 GGAGGGCTAACTGATTTGGAAGCCCAAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT 1006
QY 181 CCAGGGTGCAATACCT 197
Dd 1007 CCAGGGTGCAATATCT 1023
RESULT 10
AAT70836
ID AAT70836 standard; cDNA; 2540 BP.
XX
AC AAT70836;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor xiap cDNA.
XX
KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;
KW AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; gene therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 34..1527
FT /*tag= a
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB001022.
XX
PR 04-AUG-1995; 95US-00511485.
PR 22-DEC-1995; 95US-00576956.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Mackenzie AE, Baird S, Liston P;
XX
DR WPI; 1997-154262/14.
XX
PT P-PSDB; AAW19581.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to
PT inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of
PT susceptibility to apoptotic disease.
XX
PS Claim 12; Page 67-68; 219pp; English.
XX
CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
CC genes (AAW70836-41) respectively code for a new class of mammalian
CC proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap
CC gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII
CC cDNA library using an X-linked sequence tag site that shows strong
CC homology with the conserved ring zinc finger domain of baculovirus CpiAP
CC and OpiAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP
CC nucleic acids can be used to express IAP polypeptides in cells and
CC animals to inhibit apoptosis, and as primers and probes to identify and
CC isolate additional IAP genes, as well as in methods for treating diseases
CC and disorders involving apoptosis (anti-apoptotic gene therapy)
XX
SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;
Query Match 87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60

Db 826 TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAGGACGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGGTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTGTTCACCTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAAGTGTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 11
AAA64901
ID AAA64901 standard; DNA; 2540 BP.
XX
AC AAA64901;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human X-linked inhibitor of apoptosis DNA.
XX
DE X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880; antisense;
KW antiinflammatory; cytostatic; tumour; ds.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 34..1527
FT /tag= a
FT /product= "X-linked inhibitor of apoptosis"
XX
PN US6087173-A.
XX
PD 11-JUL-2000.

XX
PF 09-SEP-1999; 99US-00392580.
XX
PR 09-SEP-1999; 99US-00392580.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM, Ackermann EJ;
XX
DR WPI; 2000-498201/44.
DR P-PSDB; AAY99985.

XX
PT Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
XX
PS Example 13; Col 43-48; 33pp; English.

XX
CC The present invention relates to antisense oligonucleotides designed to
CC inhibit expression of the human X-linked inhibitor of apoptosis. The
CC present sequence is the X-linked inhibitor of apoptosis DNA. Modified
CC phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more
CC effective inhibitors than unmodified oligonucleotides. The
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
CC expression in cells and tissues in vitro. The oligonucleotides are also
CC useful for treating animals or humans, prone to a disease associated with
CC X-linked inhibitor of apoptosis. The oligonucleotides may also be used
CC prophylactically to prevent infection, inflammation or tumour formation
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGACGCTT 60
Db 826 TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAGGACGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAAGTGAAGTGGTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTTAGTGAAGGTGATAAAGTAAAGTGTTCACCTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAAGTGTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 12
ABK93869
ID ABK93869 standard; cDNA; 2540 BP.
XX
AC ABK93869;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
XX
KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.

XX
OS Homo sapiens.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA001379.
XX
PR 28-SEP-2000; 2000US-00672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI; 2002-479562/51.
DR P-PSDB; ABG65663.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
PT apoptosis in a cell, for treating cancer and other proliferative
PT diseases.

XX
PS Disclosure; Fig 1; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse or
CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC cDNA sequence
XX
SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 0 U; 22 Other;
Query Match 87.4%; Score 173; DB 6; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCACTGTGGA 945
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAATACCT 197
Db 1006 CCAGGGTGCAATATCT 1022
RESULT 13
ABV94283
ID ABV94283 standard; cDNA; 2540 BP.
XX
AC ABV94283;
XX
DT 08-JAN-2003 (first entry)
XX
DE Breast carcinoma related nucleotide sequence SEQ ID NO:274.
XX
KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW ss.
XX Homo sapiens.
XX WO200246467-A2.
PN
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-IB002811.
XX
PR 08-DEC-2000; 2000US-0254090P.
PR 07-DEC-2001; 2001US-00007926.
XX
PA (IPSO-) IPSOGEN.
XX
PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
PI
XX
DR WPI; 2002-619023/66.
XX
PT Novel polynucleotide library useful in molecular characterization of a
PT carcinoma, comprising a pool of polynucleotide sequences or its
PT subsequences which are either underexpressed or overexpressed in tumor
PT cells.
XX
PS Claim 1; Page 289; 401pp; English.
XX
CC The present invention describes a polynucleotide library (I) useful in
CC the molecular characterisation of a carcinoma, comprising a pool of
CC polynucleotides or its subsequences which are either underexpressed or
CC overexpressed in tumour cells, and correspond to any of the
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC (M1) differentially expressed polynucleotide sequences which are

CC correlated with a cancer, involves obtaining a polynucleotide sample from
CC a patient, and reacting the polynucleotide sample obtained with a probe
CC immobilised on a solid support, where the probe comprises any combination
CC of the polynucleotide sequences of (I) or its expression products encoded
CC by polynucleotide sequences of (I), and detecting the reaction products.
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
CC useful for the prognosis or diagnostic of tumour, in differentiating a
CC normal cell from a cancer cell, detecting a hormone sensitive tumour
CC cell, differentiating a tumour with lymph nodes from a tumour without
CC lymph nodes, differentiating antracycline-sensitive tumours from
CC antracycline-insensitive tumours, and classifying good and poor prognosis
CC primary breast tumours. (I) is useful for large-scale molecular
CC characterisation of breast cancer that help in prediction, prognosis and
CC cancer treatment, and for detecting differentially expressed genes that
CC correlated with a cancer
XX
SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
Query Match 87.4%; Score 173; DB 6; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.1e-49;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCACTGTGGA 945
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAATACCT 197
Db 1006 CCAGGGTGCAATATCT 1022
RESULT 14
AAL53731
ID AAL53731 standard; RNA; 2540 BP.
XX
AC AAL53731;
XX
DT 07-FEB-2003 (first entry)
XX
DE X-linked inhibitor of apoptosis protein SEQ ID No 25.
XX
KW Target RNA; target RNA:support-attached test compound; flow cytometry;
KW mass spectrometry; high-throughput screening; RNA motif; ss.
XX Homo sapiens.
XX WO200283837-A1.
PN
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011758.
PF
XX
PR 11-APR-2001; 2001US-0282966P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Almstead NG;
XX
DR WPI; 2003-075534/07.
XX
PT Identifying a test compound that binds to a target RNA molecule by
PT separating the detectably labeled target RNA:support-attached test
PT compound complex from uncomplexed target RNA molecules and test compounds
PT by flow cytometry.

XX Example; Page 79-80; 131pp; English.

PS The invention relates to a novel method for identifying a test compound

XX that binds to a target RNA molecule comprising separating the detectably

CC labeled target RNA: support-attached test compound complex from

CC uncomplexed target RNA molecules and test compounds. The separating

CC process is carried out by flow cytometry and determining a structure of

CC the type of test compound of the RNA: support-attached test compound

CC complex by mass spectrometry. The method is useful for high-throughput

CC screening of libraries of compounds to identify pharmaceutical leads.

CC This polynucleotide sequence represents one of the target RNA motifs/

XX regions of the invention

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 7; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.1e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

826 TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGA 120

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGATGCTAAGTGTCTAC 180

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTGGGAAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197

Db ||||||| ||||||| ||

1006 CCAGGGTGCAAAATATCT 1022

RESULT 15

AAD49663

ID AAD49663 standard; DNA; 2540 BP.

XX

AC AAD49663;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human X-linked inhibitor of apoptosis protein (XIAP) DNA.

XX

XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;

KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;

KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;

KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;

KW haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; XIAP;

XX fungicide; human; X-linked inhibitor of apoptosis protein; gene; ds.

OS Homo sapiens.

XX

XX WO200283953-A1.

PN

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-US011757.

XX

PR 11-APR-2001; 2001US-0282965P.

XX

PA (PTCT-) PTC THERAPEUTICS INC.

XX

PI Rando R, Welch E;

XX

DR WPI; 2003-075561/07.

XX

PT Identifying a test compound that binds to a target RNA molecule for

PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,

PT diabetes, by contacting a detectably labeled target RNA molecule with a

PT library of test compounds.

XX

PS Example; Page 88-89; 152pp; English.

XX

CC The invention relates to a method for identifying a test compound that

CC binds to a target RNA molecule, which comprises contacting a detectably

CC labelled target RNA molecule with a library of test compounds under

CC conditions that permit direct binding of the labelled target RNA to a

CC member of the library of test compounds so that a detectably labeled

CC target RNA: test compound complex is formed. The method is useful for

CC screening libraries of compounds for those that are selectively bind to a

CC pre-selected target RNA. The compounds are useful for inhibiting the

CC formation of a specific bound RNA: host cell factor complexes in vivo.

CC They are also useful for treating or preventing diseases associated with

CC overproduction or decreased protein function, such as amyloidosis,

CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,

CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,

CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative

CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).

CC The invention is also used in gene therapy. The present sequence is human

CC X-linked inhibitor of apoptosis protein (XIAP) DNA. This sequence is used

CC to illustrate the method of the invention

XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;

Query Match 87.4%; Score 173; DB 7; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.1e-49;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGA 120

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCACGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGATGCTAAGTGTCTAC 180

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTGGGAAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197

Db ||||||| ||||||| ||

1006 CCAGGGTGCAAAATATCT 1022

Search completed: March 13, 2004, 04:35:14

Job time : 266 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:07:08 ; Search time 62 Seconds
(without alignments)
1772.263 Million cell updates/sec

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcaggatcggttac.....accagggtgcaataacctta 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	2100	2	US-08-511-485-9 Sequence 9, Appli
2	198	100.0	2100	4	US-09-201-936-9 Sequence 9, Appli
3	198	100.0	2100	4	US-09-011-356-9 Sequence 9, Appli
4	198	100.0	2100	4	US-09-672-717-224 Sequence 224, App
5	194.8	98.4	2691	3	US-09-212-971-9 Sequence 9, Appli
6	194.8	98.4	2691	3	US-08-800-929A-9 Sequence 9, Appli
7	194.8	98.4	2691	4	US-09-617-053A-9 Sequence 9, Appli
8	173	87.4	1588	4	US-09-239-867-3 Sequence 3, Appli
9	173	87.4	1659	4	US-09-016-434-1053 Sequence 1053, Ap
10	173	87.4	2540	2	US-08-511-485-3 Sequence 3, Appli
11	173	87.4	2540	3	US-09-392-580-1 Sequence 1, Appli
12	173	87.4	2540	4	US-09-201-936-3 Sequence 3, Appli
13	173	87.4	2540	4	US-09-023-655-900 Sequence 900, App
14	173	87.4	2540	4	US-09-011-356-3 Sequence 3, Appli
15	173	87.4	2540	4	US-09-672-717-218 Sequence 218, App
16	173	87.4	3000	4	US-09-672-717-231 Sequence 231, App
17	173	87.4	5232	3	US-09-212-971-3 Sequence 3, Appli
18	173	87.4	5232	3	US-08-800-929A-3 Sequence 3, Appli
19	173	87.4	5232	4	US-09-617-053A-3 Sequence 3, Appli
20	147.4	74.4	711	3	US-09-121-979-3 Sequence 3, Appli
21	147.4	74.4	711	3	US-09-332-319-3 Sequence 3, Appli
22	147.4	74.4	1559	4	US-09-239-867-1 Sequence 1, Appli
23	134.4	67.9	152331	3	US-09-128-155-16 Sequence 16, Appl
24	109.6	55.4	176373	3	US-09-128-155-17 Sequence 17, Appl
25	76	38.4	2563	4	US-09-016-434-1076 Sequence 1076, Ap
26	76	38.4	2563	4	US-09-023-655-894 Sequence 894, App
27	76	38.4	2601	3	US-08-569-749-3 Sequence 3, Appli

28	76	38.4	2601	5	PCT-US96-12860-3 Sequence 3, Appli
29	76	38.4	2676	2	US-08-511-485-5 Sequence 5, Appli
30	76	38.4	2676	4	US-09-201-936-5 Sequence 5, Appli
31	76	38.4	2676	4	US-09-011-356-5 Sequence 5, Appli
32	76	38.4	2676	4	US-09-672-717-220 Sequence 220, App
33	76	38.4	3076	2	US-09-205-144-1 Sequence 1, Appli
34	76	38.4	6669	3	US-09-212-971-5 Sequence 5, Appli
35	76	38.4	6669	3	US-08-800-929A-5 Sequence 5, Appli
36	76	38.4	6669	4	US-09-617-053A-5 Sequence 5, Appli
37	76	38.4	6669	4	US-09-672-717-230 Sequence 230, App
38	68	34.3	2450	4	US-09-201-936-39 Sequence 39, Appl
39	68	34.3	2474	4	US-09-011-356-39 Sequence 39, Appl
40	68	34.3	2474	4	US-09-672-717-226 Sequence 226, App
41	68	34.3	2676	3	US-09-212-971-11 Sequence 11, Appl
42	68	34.3	2676	3	US-08-800-929A-11 Sequence 11, Appl
43	68	34.3	2676	4	US-09-617-053A-11 Sequence 11, Appl
44	65.8	33.2	1435	5	PCT-US95-05922A-1 Sequence 1, Appli
45	65.8	33.2	2580	2	US-08-511-485-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 198; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCGTTACTTTTGGACATGGATATACAGTTAAACAGGACGCTT 60
|||||

Db	916	TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGACGAGTT	975
QY	61	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA	120
Db	976	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA	1035
QY	121	GGAGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGCTAC	180
Db	1036	GGAGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGCTAC	1095
QY	181	CCAGGTGCAAAATACCTA	198
Db	1096	CCAGGTGCAAAATACCTA	1113

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RESULT 2
US-09-201-936-9
; Sequence 9, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

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[illegible]

RESULT 3
US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.

```

; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-011-356-9

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	Query Match	100.0%;	Score 198;	DB 4;	Length 2100;
	Best Local Similarity	100.0%;	Pred. No. 1.6e-51;		
	Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60		
DB	916	TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAAACAAGGAGCAGCTT	975		
QY	61	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA	120		
DB	976	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA	1035		
QY	121	GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCCAGCATGCTAAGTGCTAC	180		
DB	1036	GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCCAGCATGCTAAGTGCTAC	1095		
QY	181	CCAGGGTGCAAAATACCTA	198		
DB	1096	CCAGGGTGCAAAATACCTA	1113		

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RESULT 4
US-09-672-717-224
; Sequence 224, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-672-717-224

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Query Match	100.0%;	Score 198;	DB 4;	Length 2100;
Best Local Similarity	100.0%;	Pred. NO. 1.6e-61;		
Matches 198;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

QY	1	TATGAAGCACGGATCGTTACTTTTGGAACATCGATATACTCAGTTTAAACAAGGAGCAGCTT	60
Db	916	TATGAAGCACGGATCGTTACTTTTGGAACATCGATATACTCAGTTTAAACAAGGAGCAGCTT	975

QY	61	GCAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA	120
Db	976	GCAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA	1035
QY	121	GGAGGCTCACGGATTGGAAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	180
Db	1036	GGAGGCTCACGGATTGGAAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	1095
QY	181	CCAGGTCGAAATACCTA	198
Db	1096	CCAGGTCGAAATACCTA	1113

RESULTS

US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

	Query Match	98.4%;	Score 194.8;	DB 3;	Length 2691;
	Best Local Similarity	99.0%;	Pred. No. 2.5e-60;		
	Matches 196;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60		
Dδ	1461	TATGAAGCACGGATCGTTACTTTTGGAAACATGGACATCCTCAGTTAAACAAGGAGCAGCTT	1520		
QY	61	GCAAGAGCTGGATTITATGCTTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA	120		
Dδ	1521	GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA	1580		
QY	121	GGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCCTGGACCAGCATGCTAAGTGCTAC	180		
Dδ	1581	GGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCCTGGACCAGCATGCTAAGTGCTAC	1640		
QY	181	CCAGGTCGAAAATACCTA	198		
Dδ	1641	CCAGGTCGAAAATACCTA	1658		

RESULT 6

US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander I
; APPLICANT: Liston, Peter

```

1 APPLICANT: Baird, Stephen
2 APPLICANT: Tsang, Benjamin K
3 APPLICANT: Pratt, Christine
4 TITLE OF INVENTION: DETECTION AND MODULATION OF
5 TITLE OF INVENTION: IAPS AND NAIP FOR THE D
6 TITLE OF INVENTION: DISEASE
7 NUMBER OF SEQUENCES: 17
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Clark & Elbing LLP
10 STREET: 176 Federal Street
11 CITY: Boston
12 STATE: MA
13 COUNTRY: USA
14 ZIP: 02110
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FastSEQ for Windows Version 2.0
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/800,929A
22 FILING DATE: 13-FEB-1997
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 60/030,590
26 FILING DATE: 14-NOV-1996
27 APPLICATION NUMBER: 60/017,354
28 FILING DATE: 26-APR-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Bieker-Brady, Kristina
31 REGISTRATION NUMBER:
32 REFERENCE/DOCKET NUMBER: 07891/009001
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 617-428-0200
35 TELEFAX: 617-428-7045
36 TELEX:
37 INFORMATION FOR SEQ ID NO: 9:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 2691 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: cDNA
44 US-08-800-929A-9

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Query Match	98.4%;	Score 194.8;	DB 3;	Length 2691;
Best Local Similarity	99.0%;	Pred. No. 2.6e-60;		
Matches 196;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	TATGAAGCACGGATCGTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60	
DB	1461	TATGAAGCACGGATCGTTACTTTTGGACATGGACATCCTCAGTTAAACAAGGAGCAGCTT	1520	
QY	61	GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA	120	
DB	1521	GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGCGATAAAGTGAAGTGTCTTCCACTGTGGA	1580	
QY	121	GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	180	
DB	1581	GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	1640	
QY	181	CCAGGGTGCAAAATACCTA	198	
DB	1641	CCAGGGTGCAAAATACCTA	1658	

RESULT 7

US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2691
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 98.4%; Score 194.8; DB 4; Length 2691;
Best Local Similarity 99.0%; Pred. No. 2.6e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
Db 1461 TATGAGCAGCGATCGTTACTTTTGGAAACATGGACATCTCAGTTAAACAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580

QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 1640

QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658

RESULT 8
US-09-239-867-3
Sequence 3, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1588
TYPE: DNA
ORGANISM: Homo sapiens
US-09-239-867-3

Query Match 87.4%; Score 173; DB 4; Length 1588;
Best Local Similarity 92.4%; Pred. No. 1.5e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
Db 826 TATGAGCAGCGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 9
US-09-016-434-1053
Sequence 1053, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1053:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1016687
US-09-016-434-1053

Query Match 87.4%; Score 173; DB 4; Length 1659;
Best Local Similarity 92.4%; Pred. No. 1.5e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60
Db 874 TATGAGCAGCGATCGTTACTTTTGGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 933

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 934 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGAAGTGAAGTCTTCCACTGTGGA 993

QY 121 GGAGGGCTCAGCGATTGGAGCCCAAGTGAAGACCCCTGGGACGAGCATGCTAAGTGCTAC 180
Db 994 GGAGGGCTAAGTGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1053

Qy 181 CCAGGGTGCAAAATACCT 197
Db 1054 CCAGGGTGCAAAATATCT 1070

RESULT 10
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGATGAATAAGTAAAGTGCTTCCACTGTGGA 945

Qy 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 11
US-09-392-580-1

; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRES
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match 87.4%; Score 173; DB 3; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGATGAATAAGTAAAGTGCTTCCACTGTGGA 945

Qy 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGCCCTGGGACCAGCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 1005

Qy 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 12
US-09-201-936-3
; Sequence 3, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)..(2540)
; OTHER INFORMATION: N may be any nucleotide

US-09-201-936-3

Query Match 87.4%; Score 173; DB 4; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGCCCTGGGACCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGGACCATGCTAAGTGCTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 13

US-09-023-655-900
; Sequence 900, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 900:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI184319
US-09-023-655-900

Query Match

87.4%; Score 173; DB 4; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGGAAGCCAAAGTGAAGCCCTGGGACCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGGACCATGCTAAGTGCTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 14

US-09-011-356-3
; Sequence 3, Application US/09011356A
; Patent No. 6656704
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3

Query Match 87.4%; Score 173; DB 4; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
Db 826 TATGAAGCAGCGATCGTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAGTGAAGTGCTTCCACTGTGGA 945
QY 121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGCCCTGGGACCATGCTAAGTGCTAC 180
Db 946 GGAGGGCTAAGTGAAGCCCAAGTGAAGCCCTGGGACCATGCTAAGTGCTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 15

US-09-672-717-218
; Sequence 218, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2540)
; OTHER INFORMATION: n=a,t,c, or g

US-09-672-717-218

Query Match	87.4%;	Score 173;	DB 4;	Length 2540;
Best Local Similarity	92.4%;	Pred. NO. 1.9e-52;		
Matches 182;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;

QY	1	TATGAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAACAGGAGCAGCTT	60
Db	826	TATGAGCAGCGATCGTTACTTTTGGACATGGATATACTCAGTTAACAGGAGCAGCTT	885
QY	61	GCAAGAGCTGGATTTTATGCTTTAGGTGAGCGGATAAAGTGAAGTGCTTCCACTGTGGA	120
Db	886	GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATAAAGTAAAGTGCTTTCACTGTGGA	945
QY	121	GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	180
Db	946	GGAGGGCTAACTGATTGGAAGCCCAAGTGAAGACCCCTTGGGACACACATGCTAATGGTAT	1005
QY	181	CCAGGGTGCAAAATACCT	197
Db	1006	CCAGGGTGCAAAATATCT	1022

Search completed: March 13, 2004, 06:26:52
Job time : 63 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:27:28 ; Search time 207 Seconds
(without alignments)
3521.528 Million cell updates/sec

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcacggtacgttac.....accagggtgcaaataccta 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243257 seqs, 1840798884 residues
Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA: *
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq: *
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq: *
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq: *
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq: *
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq: *
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq: *
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq: *
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: *
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	198	100.0	2100	9	US-09-201-936-9	Sequence 9, Appli
2	194.8	98.4	2691	9	US-09-974-592-9	Sequence 9, Appli
3	173	87.4	1659	15	US-10-305-720-1053	Sequence 1053, Ap
4	173	87.4	2404	9	US-09-964-899-38	Sequence 38, Appli
5	173	87.4	2540	9	US-09-201-936-3	Sequence 3, Appli
6	173	87.4	2540	14	US-10-007-926A-274	Sequence 274, App
7	173	87.4	5232	9	US-09-974-592-3	Sequence 3, Appli
c	134.4	67.9	152331	13	US-10-095-407-16	Sequence 16, Appli
9	109.6	55.4	176373	13	US-10-095-407-17	Sequence 17, Appli
c	76	38.4	255	14	US-10-102-524-906	Sequence 906, App
11	76	38.4	2563	15	US-10-305-720-1076	Sequence 1076, Ap
12	76	38.4	2601	14	US-10-232-286-3	Sequence 3, Appli
13	76	38.4	2676	9	US-09-201-936-5	Sequence 5, Appli
14	76	38.4	2916	12	US-10-240-425-1436	Sequence 1436, Ap
15	76	38.4	3076	9	US-09-954-456-1635	Sequence 1635, Ap

16	76	38.4	3076	9	US-09-954-531-16	Sequence 16, Appli
17	76	38.4	3076	14	US-10-197-290-1	Sequence 1, Appli
18	76	38.4	3076	15	US-10-388-263-157	Sequence 157, App
19	76	38.4	3164	14	US-10-141-618-5	Sequence 5, Appli
20	76	38.4	3165	14	US-10-269-909-5	Sequence 5, Appli
21	76	38.4	3734	14	US-10-353-461-7	Sequence 7, Appli
22	76	38.4	5844	10	US-09-971-392-253	Sequence 253, App
23	76	38.4	5857	14	US-10-247-671-18	Sequence 18, Appli
24	76	38.4	6669	9	US-09-974-592-5	Sequence 5, Appli
25	68	34.3	2450	9	US-09-201-936-39	Sequence 39, Appli
26	68	34.3	2676	9	US-09-974-592-11	Sequence 11, Appli
27	66	33.3	7990	14	US-10-311-455-131	Sequence 131, App
28	66	33.3	7990	14	US-10-240-452-7	Sequence 7, Appli
29	65.8	33.2	1435	8	US-08-464-588-1	Sequence 1, Appli
30	65.8	33.2	1435	14	US-10-323-643-1	Sequence 1, Appli
31	65.8	33.2	2531	14	US-10-207-655-199	Sequence 199, App
32	65.8	33.2	2580	9	US-09-201-936-7	Sequence 7, Appli
33	65.8	33.2	2589	14	US-10-232-286-1	Sequence 1, Appli
34	65.8	33.2	3496	14	US-10-153-668-337	Sequence 337, App
35	65.8	33.2	3532	9	US-09-880-107-3354	Sequence 3354, Ap
36	65.8	33.2	3532	15	US-10-464-158-1	Sequence 1, Appli
37	65.8	33.2	3732	9	US-09-974-592-7	Sequence 7, Appli
38	65.8	33.2	4614	10	US-09-814-353-19934	Sequence 19934, A
39	61	30.8	2862	14	US-10-232-286-13	Sequence 13, Appli
40	61	30.8	3151	9	US-09-974-592-13	Sequence 13, Appli
41	59.4	30.0	2416	9	US-09-201-936-41	Sequence 41, Appli
42	56.4	28.5	3773	14	US-10-041-859-1	Sequence 1, Appli
c	43	54.8	7990	14	US-10-311-455-132	Sequence 132, App
c	44	54.8	7990	14	US-10-240-452-8	Sequence 8, Appli
45	53.2	26.9	843	14	US-10-244-586-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 100.0%; Score 198; DB 9; Length 2100;
Best Local Similarity 100.0%; Pred. No. 9.5e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCACGATCGTTACTTTTGGAAACATGGATATCTCAGTTAAACAGGACGCTT 60
Db 916 TATGAAGCACGATCGTTACTTTTGGAAACATGGATATCTCAGTTAAACAGGACGCTT 975

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 976 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 1035
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 180
Db 1036 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 1095
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1096 CCAGGGTGCAAAATACCTA 1113

RESULT 2
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9
Query Match 98.4%; Score 194.8; DB 9; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.4e-57;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 1520
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 1580
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 180
Db 1581 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
Db 1641 CCAGGGTGCAAAATACCTA 1658
RESULT 3
US-10-305-720-1053
; Sequence 1053, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26

; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1053
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1016687
US-10-305-720-1053

Query Match 87.4%; Score 173; DB 15; Length 1659;
Best Local Similarity 92.4%; Pred. No. 5.1e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
Db 874 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 933
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 993
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 180
Db 994 GGAGGGCTCACTGATTGGAAGCCAGTGAAGACCCCTGGGACACACATGCTAAATGGTAT 1053
QY 181 CCAGGGTGCAAAATACCT 197
Db 1054 CCAGGGTGCAAAATATCT 1070

RESULT 4
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 87.4%; Score 173; DB 9; Length 2404;
Best Local Similarity 92.4%; Pred. No. 6e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAGGAGCAGCTT 60
Db 827 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTT 886
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATATAAAGTGAAGTGTCTTCCACTGTGGA 946
QY 121 GGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACAGCATGCTAAGTGCTAC 180
Db 947 GGAGGGCTCACTGATTGGAAGCCAGTGAAGACCCCTGGGACACACATGCTAAATGGTAT 1006

QY 181 CCAGGCTGCAATACCT 197
| | | | | | | | | | | | | | | | | |
Db 1007 CCAGGCTGCAATATCT 1023

RESULT 5

US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 87.4%; Score 173; DB 9; Length 2540;
Best Local Similarity 92.4%; Pred. No. 6.2e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
| | | | | | | | | | | | | | | | | |
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
| | | | | | | | | | | | | | | | | |
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAC 180
| | | | | | | | | | | | | | | | | |
Db 946 GGAGGGCTAACTGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAT 1005

QY 181 CCAGGCTGCAATACCT 197
| | | | | | | | | | | | | | | | | |
Db 1006 CCAGGCTGCAATATCT 1022

RESULT 6

US-10-007-926A-274
; Sequence 274, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNEAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 274
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4)
; OTHER INFORMATION: gene.
US-10-007-926A-274

Query Match 87.4%; Score 173; DB 14; Length 2540;
Best Local Similarity 92.4%; Pred. No. 6.2e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCGTTACTTTTGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60
| | | | | | | | | | | | | | | | | |
Db 826 TATGAAGCACGGATCGTTACTTTTGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120
| | | | | | | | | | | | | | | | | |
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945

QY 121 GGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAC 180
| | | | | | | | | | | | | | | | | |
Db 946 GGAGGGCTAACTGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAGTGTCTAT 1005

QY 181 CCAGGCTGCAATACCT 197
| | | | | | | | | | | | | | | | | |
Db 1006 CCAGGCTGCAATATCT 1022

RESULT 7

US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin X
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match	87.4%;	Score 173;	DB 9;	Length 5232;
Best Local Similarity	92.4%;	Pred. No. 8.5e-50;		
Matches 182;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;
QY	1	TATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTTAAACAAGGAGCAGCTT	60	
DB	826	TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT	885	
QY	61	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGGGATAAAGTGAAGTGCCTCCACTGTGGA	120	
DB	886	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACCTGTGGA	945	
QY	121	GGAGGCTCAGGGATTGGAAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGCCTAC	180	
DB	946	GGAGGCTAACTGATTGGAAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTAAATGGTAT	1005	
QY	181	CCAGGCTGCAANTACCT	197	
DB	1006	CCAGGCTGCAAAATATCT	1022	

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RESULT 8
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Publication No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-16

```

Query Match	Score 134.4;	DB 13;	Length 152331;
Best Local Similarity	83.2%;	Pred. No. 1.4e-35;	
Matches 164;	Conservative 0;	Mismatches 32;	Indels 1; Gaps 1;
Qy 1	TATGAAGCACCGGATCGTTACTTTTGGAA	CATGGATATACTCAGTTAA	CAAGGAGCAGCTT 60
Db 3298	TATGAAGCATGGATCATTTACTTTGGATGTGGATATATTTCAGTTAA	CAAGGAGCAGCTT 3239	
Qy 61	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGGATAAAGTGAAGTGCTTCCACTGTGGA	120	
Db 3238	TCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTTCCTCAGTGTGGA	3179	
Qy 121	GGAGGGCTACGGATTGGAAGCCAAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC	180	
Db 3178	GGGGGGCTAATGATTGGGAACCCACCGAA-AACCTTGGGGACACATAATAATGGGAT	3120	
Qy 181	CCAGGGTGCAAAATACCT	197	
Db 3119	CCANGGTGTAAATATCT	3103	

RESULT 9
US-10-095-407-17
; Sequence 17, Application US/10095407
; Publication No. US20020164330A1

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; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match          55.4%; Score 109.6; DB 13; Length 176373;
Best Local Similarity 86.4%; Pred. No. 7.5e-27;
Matches 121; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      58 CTTGCAAGAGCTGGATTTTATGCTTTTAGGTGAAGCGGATAAAAGTGAAAGTGCTTCACACTGT 117
DB      12549 CTTTCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAAGTAAAGTGCTTTCACTGT 12608

QY      118 GGAGGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCTGGGACCAGCATGCTAAGTGC 177
DB      12609 GGAGGGGGCTAACTGATTGGAAGCCCAGCGAAGACCCTGGGAACAACATGATAAATGG 12668

QY      178 TACCAGGGTGCAAATACCT 197
DB      12669 CATCCAGGGTGTAATATCT 12688

RESULT 10
US-10-102-524-906/c
; Sequence 906, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-906

Query Match          38.4%; Score 76; DB 14; Length 255;
Best Local Similarity 67.9%; Pred. No. 2.5e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY      42 AGTTAACAGGACGAGCTTGCAAGAGCTGGATTTTATGCTTTTAGGTCAAGGCGATAAAGT 101
DB      223 AGTTAATCCTGAGCAGCTTGCAAGTGGGGTTTTTATTATGCGGTAAACAGTGATGATGT 164

QY      102 GAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGGAAGCCCAACTGAAGACCCCTGGGA 161
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Db 163 CAAATGCTTTTCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 104

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAATACCT 197

Db 103 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 68

RESULT 11

US-10-305-720-1076

Sequence 1076, Application US/10305720

Publication No. US20040010136A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

FILE REFERENCE: PA-0002-1 CON

CURRENT APPLICATION NUMBER: US/10/305,720

PRIOR FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: 09/016,434

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1076

LENGTH: 2563

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: GenBank ID No. US20040010136A1 g1160974

US-10-305-720-1076

Query Match 38.4%; Score 76; DB 15; Length 2563;

Best Local Similarity 67.9%; Pred. No. 6.9e-16;

Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGT 101

Db 932 AGTTAATCCTGAGCAGCTTGCAAGTGCAGGTTTATTTATTTATGTTGGTAAACAGTGATGATGT 991

QY 102 GAAGTGCTTCCACTGTGGAGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGA 161

Db 992 CAAATGCTTTGCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 1051

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAATACCT 197

Db 1052 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 1087

RESULT 12

US-10-232-286-3

Sequence 3, Application US/10232286

Publication No. US20030143579A1

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBERTSON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,286

FILING DATE: 30-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2601 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-232-286-3

Query Match 38.4%; Score 76; DB 14; Length 2601;

Best Local Similarity 67.9%; Pred. No. 7e-16;

Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAAGT 101

Db 932 AGTTAATCCTGAGCAGCTTGCAAGTGCAGGTTTATTTATTTATGTTGGTAAACAGTGATGATGT 991

QY 102 GAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGA 161

Db 992 CAAATGCTTTGCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 1051

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAATACCT 197

Db 1052 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 1087

RESULT 13

US-09-201-936-5

Sequence 5, Application US/09201936

Publication No. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: PCT/IB96/01022

EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-12-22

EARLIER APPLICATION NUMBER: 08/511,485

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 2676

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (2470)...(2470)

OTHER INFORMATION: N may be any nucleotide

FEATURE:

NAME/KEY: variation

LOCATION: (2476)...(2476)

OTHER INFORMATION: N may be any nucleotide

FEATURE:

NAME/KEY: variation
LOCATION: (2483)...(2483)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2602)...(2602)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 38.4%; Score 76; DB 9; Length 2676;
Best Local Similarity 67.9%; Pred. No. 7.1e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTAGGTGAAGGCGATAAAGT 101
Db 998 AGTTAAATCCTGAGCAGCTTGCAAGTGCGGGTTTATTATGCTGCTAACAGTGATGATGT 1057

QY 102 GAAGTGCTTCCACTGTGAGGAGGGCTCACGGATTGGAAGCCAAAGTGAAGCCCTGGGA 161
Db 1058 CAAATGCTTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1117

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAAATACCT 197
Db 1118 TCAACATGCCAAGTGCTTCCAAAGGTGTGAGTACTT 1153

RESULT 14
US-10-240-425-1436
Sequence 1436, Application US/10240425
Publication No. US20040033502A1
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 1436
LENGTH: 2916
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 U45878
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(2907)
OTHER INFORMATION: n = a or c or g or t
US-10-240-425-1436

Query Match 38.4%; Score 76; DB 12; Length 2916;
Best Local Similarity 67.9%; Pred. No. 7.3e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTAGGTGAAGGCGATAAAGT 101
Db 1258 AGTTAAATCCTGAGCAGCTTGCAAGTGCGGGTTTATTATGCTGGGTAAACAGTGATGATGT 1317

QY 102 GAAGTGCTTCCACTGTGAGGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGA 161
Db 1318 CAAATGCTTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1377

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAAATACCT 197

Db 1378 TCAACATGCCAAGTGCTTCCAAAGGTGTGAGTACTT 1413

RESULT 15
US-09-954-456-1635
Sequence 1635, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1635
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 38.4%; Score 76; DB 9; Length 3076;
Best Local Similarity 67.9%; Pred. No. 7.5e-16;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTAGGTGAAGGCGATAAAGT 101
Db 1534 AGTTAAATCCTGAGCAGCTTGCAAGTGCGGGTTTATTATGCTGGGTAAACAGTGATGATGT 1593

QY 102 GAAGTGCTTCCACTGTGAGGAGGGCTCACGGATTGGAAGCCAAAGTGAAGACCCCTGGGA 161
Db 1594 CAAATGCTTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGGT 1653

QY 162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAAATACCT 197
Db 1654 TCAACATGCCAAGTGCTTCCAAAGGTGTGAGTACTT 1689

Search completed: March 13, 2004, 06:34:01
Job time : 208 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2004, 04:02:03 ; Search time 2177.5 Seconds
(without alignments)
2715.367 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcacggtacgttac.....accagggtgcaaataccta 198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
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- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176.8	89.3	773	14	CD350778
2	168	84.8	628	9	AI573382
3	149	75.3	1805	11	BC039318
4	149	75.3	1851	11	BC056914

5	147.4	74.4	1789	11	BC046168
6	108	54.5	617	10	BB663325
7	103.4	52.2	504	10	BB650856
8	100.8	50.9	318	10	BF659610
9	98	49.5	334	12	BM220130
10	98	49.5	584	13	BQ552032
11	92.2	46.6	1177	12	BM805359
12	90.2	45.6	536	9	AU123207
13	88.2	44.5	791	14	CF222542
14	87	43.9	373	13	BY662508
15	85.2	43.0	849	28	BZ242580
16	84.2	42.5	716	9	AV706807
17	81.8	41.3	1472	29	AY398945
18	81.8	41.3	1494	29	AY398943
19	80.4	40.6	721	29	CE100865
20	76.2	38.5	663	13	BU658508
21	76	38.4	341	10	AW375598
22	76	38.4	354	10	AW375594
23	76	38.4	402	10	AW846507
24	76	38.4	531	10	AW375599
25	76	38.4	532	10	AW846425
26	76	38.4	546	10	AW846421
27	76	38.4	571	10	AW375649
28	76	38.4	582	10	AW846337
29	76	38.4	590	10	BE268377
30	76	38.4	621	10	AW375648
31	76	38.4	680	10	AW375625
32	76	38.4	886	13	BQ652590
33	76	38.4	1799	29	AY420753
34	75.2	38.0	269	10	BE506790
35	72.4	36.6	690	29	CE697566
36	71.2	36.0	275	29	CG545804
37	70.4	35.6	1748	29	AY420754
38	69.2	34.9	567	12	BI961039
39	69	34.8	735	14	CD284353
40	68.4	34.5	420	28	AQ011995
41	68	34.3	323	10	BE847058
42	68	34.3	385	10	BE851680
43	68	34.3	450	14	CA559631
44	68	34.3	557	9	AA197349
45	68	34.3	586	14	CF913919

ALIGNMENTS

RESULT 1	CD350778	773 bp	linear	EST 09-JUL-2003
LOCUS	UI-M-GIO-cgh-g-23-0-UI.r1	NIH_BMAP_GIO	Mus musculus	CDNA clone
DEFINITION	IMAGE:6853392 5', mRNA sequence.			
ACCESSION	CD350778	GI:31142365		
VERSION	EST.			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 773)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library prepared by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: pYX-5.			

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6853392"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_G10"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 89.3%; Score 176.8; DB 14; Length 773;
Best Local Similarity 96.3%; Pred. No. 8.1e-45;
Matches 181; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 GGATCGTTACTTTTGGACATGGATATACCTCAGTTAAACAGGAGCAGCTTGCAGAGCTG 70
|||||
Db 1 GGATCGTTACTTTTGGACATGGACATCCTCAGTTAAACAGGAGCAGCTTGCAGAGCTG 60
|||||

QY 71 GATTTTATGTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCA 130
|||||
Db 61 GATTTTATGTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCA 120
|||||

QY 131 CGGATTGGAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTACCCAGGGTGCA 190
|||||
Db 121 CGGATTGGAGCCCAAGTGAAGACCCCTGGGACCAGCATGCGAAGTGTGTACCCAGGGTGCA 180
|||||

QY 191 AATACCTA 198
|||||
Db 181 AATACCTA 188
|||||

RESULT 2
AI573382/c

LOCUS AI573382 628 bp mRNA linear EST 16-APR-1999
DEFINITION mn83e12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ;, mRNA sequence.
ACCESSION AI573382
VERSION AI573382.1 GI:4536756
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
TITLE Contact: Marra M/WashU-NCI Mouse EST Project 1999
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

FEATURES
source

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 440.
Location/Qualifiers
1. 628
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse Tcell 937311"
/note="Organ: blood; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3,"

ORIGIN

Query Match 84.8%; Score 168; DB 9; Length 628;
Best Local Similarity 93.4%; Pred. No. 4.4e-42;
Matches 185; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
|||||
Db 604 TATGAAGCACGGATCGTTACTTTTGGNACATGGACATCCTCAGTTACAAAGGAGCAGCTT 545
|||||

QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
|||||
Db 544 GCAAGAGCT-GATTTTATGCTTTAGTTGAAGCGGATAAAGTGAAGTGTCTTCACTGTGGA 486
|||||

QY 121 GGAGGGCTCAGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
|||||
Db 485 GGAGGGCTCAGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCGAAGTGGTAC 426
|||||

QY 181 CCAGGGTGCAATACCTA 198
|||||
Db 425 NCAGGGTGCAATACCTA 408
|||||

RESULT 3
BC039318

LOCUS BC039318 1805 bp mRNA linear HTC 18-NOV-2002
DEFINITION Homo sapiens, Similar to baculoviral IAP repeat-containing 8, clone
IMAGE:5269405, mRNA.
ACCESSION BC039318
VERSION BC039318.1 GI:25058167
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1805)
Strausberg,R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 74 Row: h Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: frame shifted.

Location/Qualifiers
1. 1805
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269405"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN
Query Match 75.3%; Score 149; DB 11; Length 1805;
Best Local Similarity 84.8%; Pred. No. 7.6e-36;
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGGATCGTTACTTTTGGACATGATATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1028 TATGAAGCAGCGGCTCATTTACTTTTGGACATGATGTAATCCGTTAAACAAGGAGCAGCTT 1087
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
|||||
Db 1088 GCAAGAGCTGGATTTATGCTATAGGTCAAGAGGATAAAGTACAGTGTCTTCACTGTGGA 1147
|||||

QY 121 GGAGGGTTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTCTAC 180
|||||
Db 1148 GGAGGGGTAGCCAACTGGAGGCCCAAGGAGATCCTTGGGAACAGCATGCTAATGTGTAT 1207
|||||

QY 181 CCAGGGTGCATAATACCT 197
|||||
Db 1208 CCAGGTTGCAATATCT 1224
|||||

RESULT 4
BC056914
LOCUS
DEFINITION
BC056914 1851 bp mRNA linear HTC 16-SEP-2003
Homo sapiens baculoviral IAP repeat-containing 8, mRNA (cDNA clone IMAGE:5742924).

ACCESSION
BC056914
VERSION
BC056914.1 GI:34784469
KEYWORDS
HTC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1851)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1851)
Strausberg, R.
Direct Submission
Submitted (25-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 119 Row: h Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16974127
This clone has the following problem: retained intron.

Location/Qualifiers
1. 1851
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742924"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN
Query Match 75.3%; Score 149; DB 11; Length 1851;
Best Local Similarity 84.8%; Pred. No. 7.7e-36;
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGATATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1062 TATGAAGCAGCGCTCATTTACTTTTGGACATGGATGTAATCCGTTAAACAAGGAGCAGCTT 1121
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTCCACTGTGGA 120
|||||
Db 1122 GCAAGAGCTGGATTTATGCTATAGGTCAAGAGGATAAAGTACAGTGTCTTCACTGTGGA 1181
|||||

QY 121 GGAGGGCTCAGCGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGTCTAC 180
|||||
Db 1182 GGAGGGCTAGCCAACTGGAGGCCCAAGGAGATCCTTGGGAACAGCATGCTAATGTGTAT 1241
|||||

QY 181 CCAGGGTGCATAATACCT 197
|||||
Db 1242 CCAGGTTGCAATATCT 1258
|||||

RESULT 5
BC046168

GAGAGAGAGAGGATCCAGAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATCCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 54.5%; Score 108; DB 10; Length 617;
Best Local Similarity 91.9%; Pred. No. 4.1e-23;
Matches 114; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 75 TTATGCTTTAGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGA 134
|||
Db 108 TGACACCTAAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGA 167
|||

QY 135 TTGGAAGCCAAAGTGAAGACCCCTGGGACCGCATGCTAAGTGTACCCAGGGTGCAATA 194
|||
Db 168 TTGGAAGCCAAAGTGAAGACCCCTGGGACCGCATGCTAAGTGTACCCAGGGTGCAATA 227
|||

QY 195 CCTA 198
|||
Db 228 CCTA 231

RESULT 7

BB650856 504 bp mRNA linear EST 26-OCT-2001
LOCUS BB650856 RIKEN full-length enriched, 0 day neonate cerebellum Mus
DEFINITION musculus cDNA clone C230036005 5', mRNA sequence.

ACCESSION BB650856
VERSION BB650856.1 GI:16485110
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

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Location/Qualifiers
1. .504
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="C230036005"
/tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATTCGAGTTAATTAAATCCCTCCCCCCCC 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATCCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 52.2%; Score 103.4; DB 10; Length 504;
Best Local Similarity 93.9%; Pred. No. 1.1e-21;
Matches 107; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 85 GGTGAAGCGGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA 144
|||
Db 207 GGNGAAGCGGATAAAGTGAAGTGCTTTCACCTGGGAGGAGGGCTCACGGATTGGAAGCCA 266
|||

QY 145 AGTGAAGACCCCTGGGACCGATGCTAAGTGTACCCAGGGTGCAATACCTA 198
|||
Db 267 AGTGAAGACCCCTGGGACCGATGCTAAGTGTACCCAGGGTGCAATACCTA 320
|||

RESULT 8

BF659610/c
LOCUS BF659610 318 bp mRNA linear EST 29-DEC-2000
DEFINITION uz88e12.x1 NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:3676174 3', similar to SW:1AP3_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3', mRNA sequence.

ACCESSION BF659610
VERSION BF659610.1 GI:11924744
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1436942
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 226.
Location/Qualifiers
1. .318
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3676174"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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ORIGIN

Query Match 50.9%; Score 100.8; DB 10; Length 318;
Best Local Similarity 93.8%; Pred. No. 5.6e-21;
Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 53 AGCAGCTTGCAGAGCTGGATTATGCTTTAGTGAAGCGATGAAGTGAAGTGTCC 112
Db 317 AGCAGCTTGCAGAGCTGGATTATGCTTTAGTGAAGCGATGAAGTGAAGTGTCC 258
QY 113 ACTGTGGAGGAGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCA 164
Db 257 ACTGTGGAGGAGGCTCTCGGATTGGAAGCCCAAGTGAAGACCCCTGGACCA 206

RESULT 9
BM220130/c
LOCUS
DEFINITION
BM220130 334 bp mRNA linear EST 07-JUN-2003
C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros CDNA
Library (Long) Mus musculus cDNA clone NIA:C0935E08 IMAGE:30037975
3', mRNA sequence.
ACCESSION
BM220130
VERSION
BM220130.2 GI:31478783
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 334)
AUTHORS
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
TITLE
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
JOURNAL
Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE
21429098
PUBMED
11544199
COMMENT
On Dec 14, 2001 this sequence version replaced gi:17780130.
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nih.gov
Plate: C0935 row: E column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 334

POLYA=Yes.
Location/Qualifiers
1. .334
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:C0935E08-3"
/db_xref="taxon:10090"
/clone="NIA:C0935E08 IMAGE:30037975"
/sex="Male"
/tissue_type="Male genital ridge/mesonephros"
/dev_stage="12.5-dpc"
/lab_host="DH10B"
/clone_lib="NIA Mouse 12.5-dpc Male Genital
Ridge/Mesonephros CDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sali; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
[Invitrogen:
5'-pGACTAGTTCTAGATCGGAGCGGCCCTTTT-3'] from
1.8 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker IL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sali and NotI enzymes
and cloned into Sali/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.4 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 49.5%; Score 98; DB 12; Length 334;
Best Local Similarity 95.3%; Pred. No. 4.4e-20;
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 82 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCACGGATTGGAAG 141
Db 260 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCACGGATTGGAAG 201
QY 142 CCAAGTGAAGACCCCTGGGACCGCATGCTAAGTGTACCCAGGGT 187
Db 200 CCAAGTGAAGACCCCTGGGACCGCATGCGAAGTGTACCCAGGGT 155

RESULT 10
BQ552032/c
LOCUS
DEFINITION
BQ552032 584 bp mRNA linear EST 20-JUN-2002
H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4013A06 3', mRNA sequence.
ACCESSION
BQ552032
VERSION
BQ552032.1 GI:21452918
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 584)
AUTHORS
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,
Martin, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T.,
Kargul, G.J., Luo, A.G., Kels, J., Hide, W. and Ko, M.S.H.
TITLE
Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL
Genome Res. 12 (12), 1999-2003 (2002)
MEDLINE
22354164
PUBMED
12466305

COMMENT

Other_ESTS: H4013A06-5
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cdna/NIA_7_4k.html for details.
Plate: H4013 row: A column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 584
POLYA=Yes.

FEATURES

Location/Qualifiers
1..584
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H4013A06-3"
/db_xref="taxon:10090"
/clone="H4013A06"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: Sali; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN

Query Match 49.5%; Score 98; DB 13; Length 584;
Best Local Similarity 95.3%; Pred. No. 5.8e-20;
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAG 141
|||||
Db 260 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAG 201
|||||

QY 142 CCAAGTGAAGACCCCTGGGACACGATGCTAAGTGTACCCAGGGT 187
|||||
Db 200 CCAAGTGAAGACCCCTGGGACACGATGCTAAGTGTACCCAGGGT 155
|||||

RESULT 11

BM805359
LOCUS
DEFINITION AGENCOURT 6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
5', mRNA sequence.
ACCESSION BM805359
VERSION BM805359.1 GI:19122182
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1177)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.

FEATURES

Location/Qualifiers
1..1177
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:5728685"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_124"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN

Query Match 46.6%; Score 92.2; DB 12; Length 1177;
Best Local Similarity 88.5%; Pred. No. 5.6e-18;
Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 85 GGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA 144
|||||
Db 142 GGTGAAGGCGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTAACGTATTGGAAGCCC 201
|||||

QY 145 AGTGAAGACCCCTGGGACGATGCTAAGTGTACCCAGGGTGCAATATCT 197
|||||
Db 202 AGTGAAGACCCCTGGGACGATGCTAAGTGTATCCAGGGTGCAATATCT 254
|||||

RESULT 12

AU123207
LOCUS
DEFINITION AU123207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
sequence.
ACCESSION AU123207
VERSION AU123207.1 GI:10947923
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y., Ishii, S., Saito, K.,
Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y.,
Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

Location/Qualifiers
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM1000921"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN

Query Match 45.6%; Score 90.2; DB 9; Length 536;
Best Local Similarity 86.7%; Pred. No. 1.6e-17;
Matches 98; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 85 GGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTCAGGATGGAAGCCA 144
Db 99 GGTGAAGGTGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTAAGTGAAGGCC 158

Qy 145 AGTGAAGACCCCTGGGACCATGCTAAGTCTACCCAGGGTGCATAATACCT 197
Db 159 AGTGAANACCCCTGGGACCAACATGCTAAGTCTACCCAGGGTGCATAATATCT 211

RESULT 13
CP222542 791 bp mRNA linear EST 04-AUG-2003
LOCUS AGENCOURT_14926978 NICHG_XGC_Emb5 Silurana tropicalis cDNA clone
DEFINITION IMAGE:6981334 5', mRNA sequence.
ACCESSION CP222542
VERSION CF222542.1 GI:33423250
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis

REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14642 Row: f column: 21
High quality sequence start: 3
High quality sequence stop: 735.

FEATURES
source Location/Qualifiers
1..791
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8164"
/clone="IMAGE:6981334"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHG_XGC_Emb5"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.0 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match 44.5%; Score 88.2; DB 14; Length 791;
Best Local Similarity 65.5%; Pred. No. 8.5e-17;
Matches 129; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATCTCAGTTAACAAGGAGCAGCTT 60
Db 267 TACAATGCTCGTCTTGAGACCTTTTCATCATGGTTCATTTCAATGACAGGAAACATC 326

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGATAAAGTGAAGTCTTCCACTGTGGA 120
Db 327 GCTAAAGCTGGATTTCTATAGTATAGGTGACGGAGATGCCCAAAAGTCTTTCATGTGGG 386

Qy 121 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGGACCATGCTAAGTCTGCTAC 180
Db 387 GGAGTGTAAATTTGTGGTGGCAACAGATGATCTTGGGAAGGAGCATGCCAAGGCATAT 446

Qy 181 CCAGGGTGCATAATACCT 197
Db 447 CCTGGATGCAAGTTCCT 463

RESULT 14
BY662508 373 bp mRNA linear EST 16-DEC-2002
LOCUS BY662508 RIKEN full-length enriched, 14.5 days embryo RP/+
DEFINITION Rathke's pouches Mus musculus cDNA clone K720015L24 3', mRNA
sequence.
ACCESSION BY662508
VERSION BY662508.1 GI:27031688
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Okazaki, Y., Furuno, M., Masukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, S., Dragani, T.A.,
Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawanawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takanaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp
URL: <http://genome.gsc.riken.go.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept.
Human Genetics University of Michigan Medical School 4301
MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA)
whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source Location/Qualifiers
1..373
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K720015L24"
/tissue_type="Rathke's pouches"
/dev_stage="14.5 days embryo RP/+"
/clone_lib="RIKEN full-length enriched, 14.5 days embryo
RP/+ Rathke's pouches"

ORIGIN
Query Match 43.9%; Score 87; DB 13; Length 373;
Best Local Similarity 94.4%; Pred. No. 1.4e-16;
Matches 101; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 82 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGA-GGGCTCAGGATGGAA 140
Db 113 TTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGAGGAGGGCTCAGGATGGAA 172

Qy 141 GCCAAGTGAAGACCCCTGGGACCATGCTAAGTCTACCCAGGGT 187
Db 173 GCCAAGTGAAGACCCCTGGGACCATGCTAAGTCTACCCAGGGT 219

RESULT 15
BZ242580 849 bp DNA linear GSS 12-OCT-2002
LOCUS CH230-252D1.TVB CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-252D1, genomic survey sequence.
ACCESSION BZ242580
VERSION BZ242580.1 GI:23902844
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K.,
Shvartsbeyn, A., Gebregiorgis, S., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-252D1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 252 row: D column: 1
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..849
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-252D1"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 43.0%; Score 85.2; DB 28; Length 849;
Best Local Similarity 96.7%; Pred. No. 7.8e-16;
Matches 87; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATCTCAGTTAACAAGGAGCAGCTT 60
Db 197 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATCTCAGTTAACAAGGAGCAGCTT 256

Qy 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAA 90
Db 257 GCAAGAGCTGGATTTTATGCTTTAGGTGAA 286

Search completed: March 13, 2004, 06:24:41
Job time: 2179.5 secs